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11
                                                                                                                                March 18, 2003, 08:27:02 ; Search time 32.5 Seconds
    (without alignments)
    49.200 Million cell updates/sec
                GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                          908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Listing first 45 summaries
                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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66
1 DNDISPFSGDGQ 12
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# 7. (SIDSI)/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\* 2. (SIDSI)/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\* 3. (SIDSI)/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\* 4. (SIDSI)/gcgdata/geneseqy-embl/AA1981.DAT:\* 5. (SIDSI)/gcgdata/geneseqy-embl/AA1981.DAT:\* 6. (SIDSI)/gcgdata/geneseqy-embl/AA1981.DAT:\* 6. (SIDSI)/gcgdata/geneseqy-embl/AA1981.DAT:\* 7. (SIDSI)/gcgdata/geneseqy-embl/AA1980.DAT:\* 7. (SIDSI)/gcgdata/geneseqy-embl/AA1980.DAT:\* 7. (SIDSI)/gcgdata/geneseqy-embl/AA1980.DAT:\* 7. (SIDSI)/gcgdata/geneseqy-embl/AA1980.DAT:\* 7. (SIDSI)/gcgdata/geneseqy-embl/AA1980.DAT:\* 7. (SIDSI)/gcgdata/geneseqy-embl/AA1990.DAT:\* 7. (SIDSI)/gcgdata/geneseqy-embl/AA1990.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES |        | DB ID Description   | AAO20372 |          |          | 23 AAU93726 | 23 AA020379 | 23 AAU93703 |          | 7 23 AAU93681 Dental product bon |          | 1 1 1 1 1 1 1 1 1 |
|-----------|--------|---------------------|----------|----------|----------|-------------|-------------|-------------|----------|----------------------------------|----------|-------------------|
| ď         | Oilery | e Match Length DB I | 100.0 12 | 100.0 15 | 100.0 15 |             | 100.0 23    |             | 100.0 40 | 100.0 97                         | 100.0 97 |                   |
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| Truncated phosphat Human osteoregulin Human osteoregulin Phosphatonin polyp Human phosphatonin Human osteoregulin Human osteoregulin C-terminal amidate Dental product bon C-terminal amidate Dental product bon Peptide of matrix Rat osteoregulin. Mouse osteoregulin. Human OOMI calcium Dental product bon Peptide of matrix Human polypeptide, Novel human diagno Hammophilus paraga Hammophilus paraga | Novel human<br>Novel human<br>C-terminal e<br>C-terminal e<br>Mouse type I<br>Mycobacteri<br>Mycobacteri<br>Mycobacteri<br>Mycobacteri<br>Mycobacteri<br>Mycobacteri<br>Mycobacteriu | A.  if #1.  binding motif; calcium binding motif; bone loss; renal phosphate excretion; teoclast; dental tissue; skeletal loss; reducing bone loss, is capable of   |
|---|--|---|
| AAB62669 AAB82922 AAB82920 AAB62689 AAB62689 AAB682923 AAB82923 AAAB82921 AAAB23725 AAA033706 AAAB82919 AAC13306 AAAB82919 AAAB82919 AAAB868384   | ABG2504<br>AAU93723<br>AAU93723<br>AAX72963<br>AAX72963<br>AAY04931<br>AAU36366<br>AAY04931<br>ABB68973<br>AAW00777  | 12 A mot itif; os; cos for  |
| 2009 22 23 23 23 23 23 23 23 23 23 23 23 23   |  | peptide;<br>t entry)<br>um bindir<br>otif; int<br>binding m<br>dontoblas<br>S-0641034<br>S-0812485<br>IO INC.<br>r RW, YC   |
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| 11111111111111111111111111111111111111  | 38   | 1<br>2<br>020372<br>020372<br>-MAY-2<br>ptide<br>ne grc<br>ycosar<br>ycosar<br>ycosar<br>ycosar<br>ycosar<br>-YCOSA<br>akness<br>1denti<br>1denti<br>1200214<br>-FEB-2<br>-AUG-2<br>-MAR-2<br>-MAR-2<br>-MAR-2<br>-MAR-2<br>-MAR-2<br>-MAR-2  |
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Gaps

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Indels

100.0%; Score 66; DB 23; 100.0%; Pred. No. 4.6e-05; ive 0; Mismatches 0;

Length 15;

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as well as the growth or recruiting of osteoblast or odontoblast cells on the surface of the new skeletal growth. AAU93681-AAU93726 represent bone growth enhancing peptides for use in dental products.
                                                                                                                                                                                                   Query Match 100.
Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                           15 AA;
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                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A PART OF THE PROPERTY OF THE 
                                                                                                                                                                The invention relates to a peptide compound capable of enhancing bone growth, and comprising 10-50 amino acids in a sequence, where the amino acids are in D- or L- conformation and the sequence comprises a motif selected from an integrin binding motif, a glycosaminoglycan binding motif and a calcium binding motif. The peptide of the invention is useful for reducing bone loss and for reducing renal phosphate excretion in an individual. The peptide is useful for promoting regeneration of alveolar bone and/or teeth, and increases the number and activity of odontoblasts for creating or preventing a condition associated with skeletal loss or weakness. This sequence represents a peptide of the calcium binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dental product; toothpaste; mouthwash; dental floss; bone growth; integrin binding motif; RGD; skeletal disease; dental disease; tooth; alveolar bone growth; osteoblast; odontoblast; osteopathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dental product useful for treating skeletal diseases e.g. dental diseases comprises a base material and a compound comprising specific amino acid in a sequence containing the integrin binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
   enhancing bone growth, and comprises an integrin binding motif, glycosaminoglycan binding motif or a calcium binding motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dental product bone growth enhancing peptide #44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; DB 23;
5. 3.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 66;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU93724 standard; peptide; 15 AA.
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                                                                                                     Claim 5; Page 13; 50pp; English.
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o
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #1 of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 AA;
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The invention relates to a peptide compound capable of enhancing bone growth, and comprising 10-50 amino acids in a sequence, where the amino acids are in D- or L- conformation and the sequence comprises a motif selected from an integrin binding motif, a glycosaminoglycan binding motif and a calcium binding motif. The peptide of the invention is useful for reducing bone loss and for reducing renal phosphate excretion in an individual. The peptide is useful for promoting regeneration of alveolar bone and/or teeth, and increases the number and activity of odontoblasts fosteoclasts that help form dental tissues. The peptide is also useful for treating or preventing a condition associated with skeletal loss or weakness. This sequence represents a C-terminal amidated synthesised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bone growth; RGD motif; integrin binding motif; calcium binding motif; glycosaminoglycan binding motif; bone loss; renal phosphate excretion; alveolar; teeth; odontoblast; osteoclast; dental tissue; skeletal loss; weakness; D00004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptide compound useful for reducing bone loss, is capable of enhancing bone growth, and comprises an integrin binding motif, glycosaminoglycan binding motif or a calcium binding motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C-terminal amidated synthesised peptide D-00004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                           AAO20377 standard; peptide; 15 AA.
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19-MAR-2001; 2001US-0812485.
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                                    4 DNDISPFSGDGQ 15
1 DNDISPFSGDGQ 12
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us-09-812-485a-42.rag

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The invention relates to a peptide compound capable of enhancing bone growth, and comprising 10-50 amino acids in a sequence, where the amino acids are in D- or L- conformation and the sequence comprises a motif selected from an integrin binding motif, a glycosaminoglycan binding motif for reducing bone loss and for reducing renal phosphate excretion is useful individual. The peptide is useful for promoting regeneration of alveolar bone and/or teeth, and increases the number and activity of odontoblasts for treating or preventing a condition associated with skeletal loss or weakness. This sequence represents a C-terminal amidated synthesised peptide D-00006 of the invention.
                                                           Bone growth; RGD motif; integrin binding motif; calcium binding motif; glycosaminoglycan binding motif; bone loss; renal phosphate excretion; alveolar; teeth; odontoblast; osteoclast; dental tissue; skeletal loss; weakness; D00006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dental product; toothpaste; mouthwash; dental floss; bone growth; integrin binding motif; RGD; skeletal disease; dental disease; tooth; alveolar bone growth; osteoblast; odontoblast; osteopathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptide compound useful for reducing bone loss, is capable of enhancing bone growth, and comprises an integrin binding motif, glycosaminoglycan binding motif or a calcium binding motif
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100.0%; Pred. No. 7.4e-05;
tive 0; Mismatches 0;
                                 C-terminal amidated synthesised peptide D-00006.
                                                                                                                                                                                                      /note= "C-terminal amide"
                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 15; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                             Blacher RW, Yoneda T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU93703 standard; peptide; 40 AA.
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19-MAR-2001; 2001US-0812485
   (first entry)
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                                                                                                                                                                         Key
Modified-site
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   31-MAY-2002
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Local St.
12;
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                                                                                                                                                                                                                                                                                                                                                                                                             Kumagai Y,
                                                                                                                                            Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to dental products such as toothpastes, mouthwash and dental floss comprising a base material and a compound which promotes bone growth. Such compounds are peptide sequences comprising 10-50 amino acids and containing an integrin binding motif such as RGD in the D- or L- form, preferably the L-configuration. The peptides of the invention are useful for treating or preventing skeletal diseases such as dental disease. The peptides enhance tooth and/or alveolar bone growth on areas where deterioration has occurred, as well as the growth or recruiting of osteoblast or adontoblast colls on the surface of the new skeletal growth. AAU933681-AAU93726 represent bone growth enhancing peptides for use in dental products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dental product useful for treating skeletal diseases e.g. dental diseases comprisss a base material and a compound comprising specific amino acid in a sequence containing the integrin binding motif
                                                                                                                                                                                                                                                                               Dental product; toothpaste; mouthwash; dental floss; bone growth; integrin binding motif; RGD; skeletal disease; dental disease; tooth; alveolar bone growth; osteoblast; odontoblast; osteopathic.
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                 Indels
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100.0%; Pred. No. 7.4e-05;
tive 0; Mismatches 0;
 Pred. No. 4.6e-05;
                 Mismatches
                                                                                                                                                      AAU93726 standard; peptide; 23 AA.
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 100.08;
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                Conservative
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                                              DNDISPFSGDGQ 12
                                                             4 DNDISPFSGDGQ 15
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 AA;
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                                                                                                                                                                                                                                                                                                                                            Synthetic.
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AAU93726
ID AAU9
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ID AAO2
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AC AAO2
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Length 23; Indels

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40 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bone growth; RGD motif; integrin binding motif; calcium binding motif; glycosaminoglycan binding motif; bone loss; renal phosphate excretion; alveolar; teeth; odontoblast; osteoclast; dental tissue; skeletal loss; weakness; matrix extracellular phosphoglycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein of matrix extracellular phosphoglycoprotein containing RGD #23
                                                                                                                                                                         Dental product useful for treating skeletal diseases e.g. dental diseases comprises a base material and a compound comprising specific amino acid in a sequence containing the integrin binding motif
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Pred. No. 0.00014;
Mismatches 0;
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                                                                                                                                  Kumagai Y;
                                                                                                                                                                                                                  6; Page 20; 44pp; English
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100.0%;
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19-MAR-2001; 2001US-0812485.
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                                                                                                               (BIGB-) BIG BEAR BIO INC
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                  Nomizu M,
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Best Local Similarity
Matches 12; Conserv
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                                                 21-FEB-2002
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        Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dental product useful for treating skeletal diseases e.g. dental diseases comprises a base material and a compound comprising specific amino acid in a sequence containing the integrin binding motif
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                                                                                                                                            of
                                                                                                                                    New peptide compound useful for reducing bone loss, is capable enhancing bone growth, and comprises an integrin binding motif, glycosaminoglycan binding motif or a calcium binding motif
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Yoneda T;
                                                                                                                                                                                                                                                                                            Disclosure; Page 12; 50pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 11; 44pp; English.
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Kumagai Y, Blacher RW,
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which promotes bone growth. Such compounds are peptide sequences comprising 10-50 amino acids and containing an integrin binding motif such as RGD in the D- or L. form, preferably the L-configuration. The peptides of the invention are useful for treating or preventing skeletal diseases such as dental disease. The peptides enhance tooth and/or alveolar bone growth on areas where deterioration has occurred, as well as the growth or recruiting of osteoblast or odontoblast cells on the surface of the new skeletal growth. AAU933681-AAU93726 represent bone growth enhancing peptides for use in dental products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bone growth; RGD motif; integrin binding motif; calcium binding motif; glycosaminoglycan binding motif; bone loss; renal phosphate excretion; alveolar; teeth; odontoblast; osteoclast; dental tissue; skeletal loss; weakness; matrix extracellular phosphoglycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein of matrix extracellular phosphoglycoprotein containing RGD #1
                                                                                                                                                                                                                                                                                    Gaps
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100.0%; Pred. No. 0.00039;
ive 0; Mismatches 0;
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19-MAR-2001; 2001US-0812485.
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                                                                                                                                                                                                                                                           Local Similarity 100.
nes 12; Conservative
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Best Local 3
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ID AA0
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97 AA;

Sequence

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                                                                                                                                                                                                                                                     Human; phosphatonin; Metastatic-tumour Excreted Phosphaturic-Element;
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e= "Casein kinase II phosphorylation site"
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te= "Casein kinase II phosphorylation site"
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/note= "Tyrosine kinase phosphorylation site"
 Length 97;
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194..197
/note= "Casein kinase II phosphorylation
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ce= "protein kinase C phosphorylation
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/note= "protein kinase C phosphorylation
                           0; Indels
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ce= "Casein kinase II phosphorylation
                                                                                                                                                                                                                         Amino acid sequence of a human phosphatonin polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ...154
te= "cell attachment tripeptide"
100.0%; Score 66; DB 23;
100.0%; Pred. No. 0.00039;
ive 0; Mismatches 0;
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/note= "myristoylation site"
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                                                                                                                                             AAY53812 standard; Protein; 430 AA
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 Query Match
Best Local Similarity
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                                                                                                                   RESULT 10
AAY53812
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The present sequence represents a phosphatonin polypeptide (also called Metastatic-tumour Excreted Phosphaturic-Element (MEPE)). The level of phosphatonin in a subject modulates Na+-dependent phosphate cotransport, vitamin D metabolism and/or bone mineralisation. The phosphatonin polypeptides, polynucleotides, vectors and antibodies are used to treat phosphate metabolism related disease. They are used for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hyperphosphatemia, or renal osteodystrophy, hyperphophatemia in renal dialysis/pre-dialysis, secondary hyperparathyrodism or osteitis fibrosa cystica, or x-linked hypophosphatemic rickets, hereditary hypophosphatemic rickets, hereditary hypophosphatemic rickets with hypercalcuis (HHRH), hypomineralised bone lesions, stunted growth in juveniles, oncogenic hypophophatemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptides involved in the regulation of phosphate metabolism useful for diagnosing and treating disorders related to phosphate
                                                                                                                                                                                                                                                                                                                                                           /note= "cAMP and cGMP dependent protien kinase
    phosphorylation site"
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266..271
/note= "myristoylation site"
                                           "myristoylation site"
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98GB-0019387
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312..314
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384..38
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409..41
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403..40
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              osteoporosis, vitamin D resistant rickets, end organ resistance, renal Fanconi syndrome, autosomal rickets, Paget's disease, kidney failure, renal tubular acidosis, cystic fibrosis or sprue. The polypeptide may also be used to manufacture combined preparations for simultaneous,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
161..192
/note= "the amino acid residues in this region are indicated incorrectly in the sequence provied in the sequence listing"
                                                                                   separate or sequential use for the treatment of phosphate metabolism disorders. A transformed osteoblast or bone cell line capable of phosphatonin overexpression is useful for the production of
                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Metastatic-tumour excreted phosphaturic element; MEPE; phosphatonin; phosphate; vitamin-D; skeletal formation; mineralization; truncated; osteopathic; antigout; cytostatic; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention relates to a novel human protein, metastatic-tumour
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osteomalacia, renal phosphate leakage, renal osteodystrophy,
                                                                                                                                                                                                           Length 430;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Truncated phosphatonin polypeptide (truncated MEPE).
                                                                                                                                                                                                           100.0%; Score 66; DB 21;
100.0%; Pred. No. 0.0021;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 12; Conservative
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                                                                                                                                                                          430 AA;
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                                                                                                                                          phosphatonin.
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hypophosphatemic rickets, hereditary hypophosphatemic rickets with hypercalcuria (HHRH), hypomineralized bone lesions, stunted growth in juveniles, oncogenic hypophosphatemic osteomalacia, renal phosphate leakage, renal osteodystrophy, osteoporosis, vitamin-D resistant rickets, end organ resistance, renal Fanconi syndrome, autosomal rickets, Paget's end organ resistance, renal tubular acidosis, cystic fibrosis or sprue. Phosphatonin polynucleotides are useful as molecular weight markers on Southern gels, as diagnostic probes for detecting the presence of a specific mRNA. Phosphatonin polypeptides are also useful for identifying agonists and antagonists, compounds which bind to phosphatonin and drug candidates for therapy of phosphate metabolism disorders. The present sequence represents a truncated form of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel osteoregulin polypeptide useful for regulating bone homeostasis, adiposity and calcification of atherosclerotic plaques comprises measuring the activity of osteoregulin - \frac{1}{2} \int_{-\infty}^{\infty} \frac{1}{
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of human osteoregulin mature polypeptide, i.e. lacking an N-terminal signal sequence. Osteoregulin is a novel protein which plays a role in regulating bone homeostasis, adiposity, and the calcification of atherosclerotic plaques. 2 Splice variants of human osteoregulin were identified (see also AAB82923). The invention provides novel osteoregulin proteins, nucleic acids which encode them, vectors, antibodies, host cells which express heterologous osteoregulins, and animal cells and mammals with a targeted disruption of an osteoregulin gene. The invention also provides screening assays
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22-SEP-2000; 2000US-234500P.
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Novel osteoregulin polypeptide useful for regulating bone homeostasis, adiposity and calcification of atherosclerotic plaques comprises measuring the activity of osteoregulin -
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to identify modulators of osteoregulin activity as well as methods of treating mammals for diseases or disorders associated with in the manufacture of a medicament for, as well as for treating, a mammal in need of regulation of bone mass and/or density, adjosty vascular flexibility, and/or atheroscierotic plaque calcification (claimed), for treating and preventing osteoporosis, and for stimulating bone repair and regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Osteoregulin; human; bone; homeostasis; adipose; calcification; atherosclerosis; osteoporosis; osteopathic; antiarteriosclerotic;
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                                                                                                                                                                                                                                                                                                                                   Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                   100.0%; Score 66; DB 22;
100.0%; Pred. No. 0.0026;
ive 0; Mismatches 0;
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/label= Mature_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB82920 standard; Protein; 525 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gowen LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-FEB-2001; 2001EP-0301768.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-FEB-2000; 2000US-185617P.
22-SEP-2000; 2000US-234500P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            De Wet JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233 DNDISPFSGDGQ 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DNDISPFSGDGQ 12
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                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human osteoregulin.
                                                                                                                                                                                                                                                                             509 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB82920;
                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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sprue. Phosphatonin polynucleotides are useful as molecular weight markers on Southern gels, as diagnostic probes for detecting the presence of a specific mRNA. Phosphatonin polypeptides are also useful for identifying agonists and antagonists, compounds which bind to phosphatonin and drug candidates for therapy of phosphate metabolism disorders. The present sequence represents the amino acid sequence of
                                                                                             the entire phosphatonin (MEPE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphatonin.
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                                                                                                                                                                                 12;
                                                                                                                          Sequence
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                                                                                                                                                    Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel human protein, metastatic-tumour excreted phosphaturic element (MEPE) or phosphatonin (modulator of phosphate and vitamin-D metabolism). The phosphatonin polypeptides, polynucleotides and specific antibodies are useful for treating a disorder of phosphate or vitamin D metabolism, skeletal formation and mineralization. Phosphatonins are used to treat hyperphosphatemia, renal osteodystrophy, secondary hyperparathyroidism, ostelits fibrosa cystica hypephosphatemic rickets, hereditary hypophosphatemic rickets with hypephosphatemic rickets, hereditary hypophosphatemic rickets with juveniles, oncogenic hypophosphatemic osteomalacia, renal phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New phosphatonin polypeptide a regulator of phosphate metabolism, for diagnosing and treating disorders of phosphate, vitamin-D metabolism, skeletal formation e.g. osteoporosis, Paget's disease, gout
                                                                                                                                                                                                             Gaps
osteoregulin gene. The invention also provides screening assays to identify modulators of osteoregulin activity as well as methods of treating mammals for diseases or disorders associated with osteoregulin activity. The modulators of activity may be useful in the manufacture of a medicament for, as well as for treating, a mammal in need of regulation of bone mass and/or density, adiposity, vascular flaxibility, and/or atherosclerotic plaque calcification (claimed), for treating and preventing osteoporosis, and for stimulating bone repair and regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Metastatic-tumour excreted phosphaturic element; MEPE; phosphatonin; phosphate; vitamin-D; skeletal formation; mineralization; truncated;
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                                                                                                                                                                             Score 66; DB 22; Length 525; Pred. No. 0.0027; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphate; vitamin-D; skeletal formation; osteopathic; antigout; cytostatic; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 133-134; 135pp; English.
                                                                                                                                                                                                                                                                                                                                            AAB62689 standard; Protein; 525 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphatonin polypeptide (MEPE).
                                                                                                                                                                              100.0%;
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99GB-0026424
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                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                            Local Similarity 100. ses 12; Conservative
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N-PSDB; AAF83764.
                                                                                                                                                  525 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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08-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                         AAB62689;
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                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphatonin of human origin and DNA encoding it for diagnosis and treatment of diseases associated with disorders of phosphate metabolism, e.g., hyperphosphaemia, arteriosclerosis, heart failure, diabetic renal disease and kidney failure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human phosphatonin; cytostatic; antidiabetic; antiinflammatory; hyperphosphaemia; arteriosclerosis; heart failure; diabetic renal disease; kidney failure; cystic fibrosis.
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                                                              Length 525;
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                                                        100.0%; Score 66; DB 22;
11arity 100.0%; Pred. No. 0.0027;
Conservative 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                           ABB08526 standard; protein; 525 AA.
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249 DNDISPFSGDGQ 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human phosphatonin.
                                                                                            Local Similarity
525 AA;
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| al Similarity<br>12; Conserv  | DNDISPFSGDGQ 12 | DNDISPFSGDGQ 260 |
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Result
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Sequence 55, Appli
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|            | 45                | 44                | 43                | 42                | 41               | 40               | 39                | 38        | 37              | 36                | 35                | 34                | 33                | 32                | 32                | 30                | 29                | 28                |
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|            | 51.5              | 51.5              | 53.0              | 53.0              | 53.0             | 53.0             | 53.0              | 53.0      | 53.0            | 53.0              | 53.0              | 53.0              | 53.0              | 53.0              | 53.0              | 53.0              | 53.0              | 54.5              |
|            | 106               | 106               | 1722              | 607               | 607              | 604              | 532               | 279       | 279             | 278               | 278               | 278               | 278               | 240               | 211               | 137               | 40                | 1784              |
|            | 4                 | 4                 | 4                 | 4                 | 4                | 4                | 4                 | 6         | N               | 4                 | 4                 | N                 | N                 | 4                 | N                 | 4                 | 4                 | 4                 |
| ALIGNMENTS | US-09-113-977C-49 | US-09-113-977C-48 | US-09-194-612A-1  | US-09-211-704A-10 | US-09-000-041A-2 | US-09-391-104-30 | US-09-294-841-2   | 5472855-6 | US-09-135-658-4 | US-08-955-424-6   | US-09-253-854-6   | US-07-849-420-6   | US-08-865-203-6   | US-09-355-166-19  | US-08-708-958-1   | US-09-036-574-4   | US-09-004-406C-16 | US-08-652-426A-2  |
|            | •                 | Sequence 48, Appl | Sequence 1, Appli | Sequence 10, Appl | 'n               | 30               | Sequence 2, Appli | 5         | -               | Sequence 6, Appli | Sequence 6, Appli | Sequence 6, Appli | Sequence 6, Appli | Sequence 19, Appl | Sequence 1, Appli | Sequence 4, Appli | Sequence 16, Appl | Sequence 2, Appli |

; MOLECULE TYPE: protein PCT-US96-01314-55 Sequence 55, Application PC/TUS9601314 GENERAL INFORMATION: APPLICATION NUMBER: PCT/US96/013
FILING DATE: 30-7AN-96
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/380,167
FILING DATE: 30-7AN-95
ATTORNEY/AGENT INFORMATION:
NAME: JOhn W. Freeman
REGISTRATION NUMBER: 29,066 TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO: COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0) REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-8906 SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA: TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES: SEQUENCE CHARACTERISTICS: CORRESPONDENCE ADDRESS ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street 1: 256 amino acids amino acid Massachusetts Y: U.S.A. M. Amin Arnaout linear METHODS FOR IDENTIFYING INTEGRIN ANTAGONISTS 56.1%; 87.5%; Richardson P.C PCT/US96/01314 00786/267001 Score 37; DB Pred. No. 56; 5. Length 256;

0,

Mismatches

1;

Indels

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US-07-637-399-1
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US-07-637-870-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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5310665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: MUTASHIGE, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2461
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5500
                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                  APPLICANT: Misset, Onno TITLE OF INVENTION: NOVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/637,870
FILING DATE: 19910104
CLASSIFICATION: 435
                                             NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                      APPLICANT:
                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lasters, Ignace
APPLICANT: Quax, Wilhemus J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Van Der Laan, Jan M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 41.
TELEFAX: 706141
                                                                                                                                                                                                                                                                                                                                         55 DDDLVPFGSDAQ 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
                 STREET:
                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                           Match 56.1%;
Local Similarity 50.0%;
les 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H: 394 amino acids
Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/07637870
               E: Morrison & Foerster
545 Middlefield Road, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  415-327-2951
                                                                                                                                                                     Lasters, Ignac
Mrabet, Nadir
                                                                                                                                Quax, Wilhelmus J.
Van Der Laan, Jan M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
                                                                                                                                                                                                   Lambeir, Anne-Marie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lambier, Anne-Marie
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                                                                                    ALTERED PH OPTIMUM
                                                                                                                                                                                   Ignace
                                                                                                  NOVEL GLUCOSE ISOMERASES WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>--</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37;
                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 394;
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RESULT 4
US-07-640-476-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/07640476 Patent No. 5376536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
            ATTORNEY/AGENT INFORMATION:
NAME: Kate H. Murashige
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 240
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 19910110
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
TELEFAX: 415-327-2951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
NAME: Murashige, Kate H.
AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 19910104
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SCHUURHUIZEN, APPLICANT: MRABET, NADIR TITLE OF INVENTION: NOVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                STREET: 545 Minus
CITY: Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: AMINO ACID STRANDEDNESS: Sir
                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 DDDLVPFGSDAQ 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Morrison & Foerster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DNDISPFSGDGQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                          94025
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                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QUAX, WILHELMUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCHUURHUIZEN, PAUL W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LUITEN, RUDOLF G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                    PatentIn Release #1.0, Version #1.25
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(415)
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50.0%;
                                                                                                                                  US/07/640,476
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                                 24615-20009.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 394;
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                                                                                                                    US-08-112-703-1
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                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/112
FILING DATE: 26-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUTAShige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4615
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
                                                                                                                                                                                                        TELEX: 706141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE: 394 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Misset, Onno TITLE OF INVENTION: NOVI TITLE OF INVENTION: ALTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                        Local Similarity hes 6; Conserv
                                                                                                                                            TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 755 Page
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
mes 6; Conserv
55 DDDLVPFGSDAQ 66
                                                                                                                                                                                                                                    TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 DNDISPFSGDGQ 12
                             1 DNDISPFSGDGQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94304-1018
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AMINO ACID
DGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Morrison & Foerster 755 Page Mill Road
                                                                                                                                                                                                                                    415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lambeir, Anne-Marie
Lasters, Ignace
Mrabet, Nadir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Van Der Laan, Jan M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quax,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                  linear
                                                                                                                                              single
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50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOVEL GLUCOSE ISOMERASES WITH ALTERED PH OPTIMUM
                                                                       56.1%;
50.0%;
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                                                                                     Score 37;
                                                                       Pred. No. 90;
                                                          Mismatches
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                                                                                     1;
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                                                                                    Length 394;
                                                        Indels
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                                                        Gaps
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RESULT 6
5290690-2
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Best Local Similarity
5: Conserve
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US-08-054-077C-2
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APPLICANT: MRABET, NADIR;LASTERS, IGNACE;STANSSENS, PATRICK;MATTHYSSENS, GASTON;WODAK, SHOSHANA;QUAX, WILHELMUS J.

TITLE OF INVENTION: METHODS AND MEANS FOR CONTROLLING THE
;STABILITY OF PROTEINS
                                                                                  ; MOLECULE TYPE: US-08-054-077C-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5290690-2
                                                                                                                                           APPLICATION NUMBER: US 07/694314
FILING DATE: 01-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, DAVID S.
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 40937
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 799 amino acids
TYPUEN: 201291
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                                           Query Match
            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: HEMLER, MARTIN E.
APPLICANT: RAMASWAMY, HEMAVATHI
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08
FILING DATE: 27-APR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
ADDRESSEE: CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 22
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: HUMAN INTEGRIN 5 SUBUNIT PROTEIN NUMBER OF SEQUENCES: 7
56.1%;
Local Similarity 87.5%;
hes 7; Conservating
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/
FILING DATE: 25-AUG-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: MASSACHUSETTS
                                                                                                                     TOPOLOGY:
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                                                                                                                                amino acid
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50.0%;
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Pred. No.
                         Score 37; DB 1; Length 799; Pred. No. 1.9e+02;
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CURRENT APPLICATION NUMBER: US/09/113,977C
CURRENT FILING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 42
LENGTH: 106
TYPE: PRT
ORGANISM: Mus musculus
US-09-113-977C-42
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Best Local Similarity
Matches 8; Conserve
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SEQ ID NO 405
LENGTH: 1198
TYPE: PRT
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                                                           Matches
                                                                           Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tsongalis, John
TITLE OF INVENTION: VIRILENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
FILE REFERENCE: 00786/361002
CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
                                                                                                                                                                                                                                                            TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ADHESION MOLECULE TITLE OF INVENTION: FUNCTION FILE REFERENCE: 100086.403
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PRIOR FILING DATE: 1997-11-25
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82 DNGIPPMSGTG
                            1 DNDISPFSGDG 11
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                                                           l Similarity
7; Conserv
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Rahme, Laurence G.
Mahajan-Miklos, Shalina
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92
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63.6%;
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57.1%;
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Pred. No.
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                                                             Mismatches
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3e+02;
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RESULT 10

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RESULT 12

US-09-134-001C-3471

Sequence 3471, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENTITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND
FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/064,964
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SEQ ID NO 41
LENGTH: 107
TYPE: PRT
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Best Local S
Matches 7
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Best Local Similarity b3.v
""" hes 7; Conservative
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APPLICANT: Doherty, Patrick
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
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TITLE OF INVENTION:
FILE REFERENCE: 1000
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TITLE OF INVENTION:
FILE REFERENCE: 100
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                                                                                                                                                                                                                                                                                                                                     Local Similarity
nes 7; Conserv
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63.6%;
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                                                                                                            AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
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RESULT 14
PCT-US95-08071-98
; Sequence 98, Application PC/TUS9508071
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TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3471
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PCT-US93-12588-98
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NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3471
LENGTH: 327
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                                                                                                                                              Matches
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APPLICATION NUMBER: US 07/998,003
FILING DATE: 29 DEC 1992
ATTORNEY/AGENT INFORMATION:
NAME: NOLand, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31811
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474.6300
                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Chicago
CITY: Chicago
TMATE: Illinois
TMSA
                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                           MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                         TELEFAX: 25-3856
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                                                                               305 DNGIPPMSGTG 315
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                                                                                                                                            Local Similarity les 7; Conserv
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                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                              1 DNDISPFSGDG 11
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63.6%;
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77.8%;
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    Mismatches

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Pred. No. 1.1e+02;
                                                                                                                                                            Score 36; I
Pred. No. 1
                                                                                                                                              Mismatches
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1.5e+02;
                                                                                                                                                                        Length 441;
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                                                                                                                                                                                                                                                                               RESULT 15
US-08-997-251-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US95-08071-98
                                                                                                                                                                                                                                Sequence 4, Application US/08997251 Patent No. 6271440 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION: APPLICANT: Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                    NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/998,003
FILING DATE: 29 DEC 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                  APPLICANT: GUBLER, FRANZ J. APPLICANT: JACOBSEN, JOHN V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 23 DEC PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 25-3856
                                                                                                                                                                                                                                                                                                                                          305 DNGIPPMSGTG 315
                                                                                              CITY: Boulder
STATE: CO
                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 6300 9
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                                                              80303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                 SD
                                                                                                                                                                      JACOBSEN, JOHN V.
VENTION: PLANT REGULATORY PROTEINS III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suzuki,
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
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                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 5;
Pred. No. 1.5e+02;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 441;
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0;

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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/997,251
FILING DATE: 23-DEC-1997
CLASSIPICATION UNBER: WO AU96/00383
FILING DATE: 21-UN-1996
PRIOR APPLICATION NATA:
APPLICATION NUMBER: AU PN6470/95
FILING DATE: 21-UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN6470/95
FILING DATE: 09-NOV-1995
PRIOR APPLICATION NUMBER: AU PN6470/95
FILING DATE: 09-NOV-1995
PRIOR APPLICATION NUMBER: AU PN6470/95
FILING DATE: 33-UN-1995
PRIOR APPLICATION NUMBER: AU PN6470/95
FILING DATE: 33-UN-1995
PRIOR APPLICATION NUMBER: AU PN6470/95
FILING DATE: 33-UN-1995
PRIOR APPLICATION NUMBER: AU PN6470/95
FILING DATE: 309-NOV-1995
FILING DATE: 30
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Database :
                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                        Sequence:
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                          US-09-812-485A-42
                                                                                                                                                                                                                                                                                                                                                                                                                                           March 18, 2003, 08:28:44; Search time 13.5 Seconds (without alignments) 85.453 Million cell updates/sec
                                                                                                                                                                                                                                                                               283224 seqs, 96134422 residues
                                                                                                                                                                                                                                                                                                                                                                        1 DNDISPFSGDGQ 12
                                                                          PIR_73:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
pir1:*
pir2:*
pir3:*
pir4:*
                                                                                                                                                                                                                                          283224
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

| 29                | 28                 | 27                 | 26                 | 25                 | 24                 | 23                 | 22       | 21      | 20                | 19                 | 18                 | 17     | 16                 | 15     | 14                 | 13     | 12                 | 11     | 10                 | 9                  | 8      | 7                 | σ      | ر.     | 4      | ω      | 2      | ь       | Result<br>No.  |   |
|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|---------|-------------------|--------------------|--------------------|--------|--------------------|--------|--------------------|--------|--------------------|--------|--------------------|--------------------|--------|-------------------|--------|--------|--------|--------|--------|---------|----------------|---|
| 37                | 37                 | 37                 | 37                 | 37                 | 37                 | 37                 | 37       | 37      | 37                | 37                 | 37                 | 37     | 37                 | 38     | 38                 | 38     | 38                 | 39     | 39                 | 39                 | 39     | 40                | 40     | 41     | 41     | 42     | 43     | 45      | Score          |   |
| 56.1              | 56.1               | 6                  | 56.1               | σ.                 | 56.1               | 6                  | 56.1     | 56.1    | 56.1              | 56.1               | 56.1               | 56.1   | 56.1               | 57.6   | 7.                 | 7.     | 7.                 | 59.1   | 59.1               | 59.1               | 59.1   | 60.6              | 60.6   | 62.1   |        | Ψ      | 65.2   | 68.2    | Query<br>Match | d |
| 1002              | 919                | 832                | 799                | 734                | 696                | 683                | 656      | 623     | 542               | 497                | 490                | 402    | 394                | 886    | 886                | 444    | 348                | 2733   | 393                | 347                | 300    | 1767              | 1758   | 886    | 337    | 420    | 629    | 913     | Length         |   |
| N                 | Н                  | N                  | 2                  | N                  | N                  | N                  | N        | Ь       | 2                 | ۲                  | N                  | ب      | Ц                  | Ν      | N                  | N      | ν                  | 2      | ນ                  | N                  | 2      | N                 | Ν      | 2      | N      | N      | N      | 2       | DB             |   |
| A56678            | RNVZCA             | C86431             | A38308             | S37998             | S44912             | D83511             | JC2005   | S33167  | T06728            | S20174             | E69066             | F48552 | ISMAXM             | AD0831 | A85905             | в83891 | C91060             | S15760 | S59499             | A83170             | H70879 | S60124            | F88559 | G65036 | S38166 | AE1857 | T39285 | D82885  | ID             |   |
| yemanuclein-alpha | DNA-directed RNA p | T5I8.5 protein - A | integrin beta-5 ch | probable serine/th | hypothetical prote | flagellar hook-ass | rin beta | inted p | pectate lyase (EC | protein kinase MEK | conserved hypothet | ∍      | xylose isomerase ( |        | hypothetical prote | ×      | hypothetical prote |        | cellulase egl1 - s | S-adenosylmethioni |        | transport protein | •      |        |        | μ.     | transm | tiple b | Description    |   |

## ALIGNMENTS

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A;Cross-references: GB:BA000019; PIDN:BAB72364.1; A;Experimental source: strain PCC 7120 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-3, A; Cross-references: EMBL: 228313; NID: 9
A; Cross-references: Exparimental source: strain $288C
A; Experimental source: J; Baladron, V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein YKR088c - yeast (Saccharomyces cerevisiae)

N;Alternate names: hypothetical protein YKR408

C;Species: Saccharomyces cerevisiae

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 19-Apr-2002

C;Accession: S38166; S42017; S39129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA RESEAULT, 177-213, 2001

DNA RESEAULT STATEMENT OF THE FILAMENTOUS NITROGEN-FIXING A; TITLE: Complete Genomic Sequence of the Filamentous Nitrogen-fixing A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Nitrogen Sequence of the Filamentous Nitrogen-fixing Nitrogen Sequence of the Filamentous Nitrogen-fixing Nitrogen Sequence of the Filamentous Nitrogen Nit
                                                                                                                                 F;138-154/Domain:
F;174-190/Domain:
F;290-306/Domain:
                                                                                                                                                                                                                           F;96-112/Domain: transmembrane #status predicted <TM1>
                                                                                                                                                                                                                                                            C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                          A; Map position: 11R
                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-337 <GAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Garcia-Cantalejo, J.; Baladron, V.; Esteban, P.F.; Santo Yeast 10, 231-245, 1994
A;Title: The complete sequence of an 18,002 bp segment of A;Reference number: S42009; MUID:94262327; PMID:8203164
A;Accession: S42017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: S38166; S42017; S3912 R;Baladron, V.; Ballesta, J.P.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL: Z27116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S38166
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-337 <BAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
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      Matches
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                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 7; Conserv
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   Conservative
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                                                                                                                                 transmembrane
                                                                                                                                                            transmembrane #status
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                                 62.1%;
66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                          16; NID:g415899; PIDN:CAA81639.1; PID:g415908
S288C
                                                                                                                              #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NID: g486572; PIDN: CAA82167.1;
Score 41; DB Pred. No. 16; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42; DB Pred. No. 13; 2; Mismatches
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, March 1994
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, M.; Yasuda, M.; Tabata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PID:g486573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSPDB:GN00179
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A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64/20; MUID:97426617; PMID:9278503
A;Accession: G65036
A;Status: preliminary; nucleic acid sequence not shown; transla
                                                                                            transport protein homolog C48B4.4 - Cae
C;Speckes: Caenorhabditis elegans
C;Date: 13-Jan-1996 #sequence_revision
C;Accession: S60124; S40724; S40725
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C;Superfamily: unassigned
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A; Residues: 1-1758 <
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C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #
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A;Experimental source: strain K-12, substrain MG1655
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C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997
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                             submitted to the EMBL Data
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger. A; Note: published errata appeared in Science 283, 35, 1999; Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession:
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70.0%;
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Pred. No. 1.4e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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A;Accession: $60124
A;Molecule type: DNA
A;Residues: 1-1767 <KER>
A;Cross-references: EMBL:229117; NID:g439247; PID:g1066912
C;Genetics:
A;Cross-references: EMBL:229117; NID:g439247; PID:g1066912
C;Genetics:
A;Map Position: III
A;Introns: 47/1; 112/3; 161/2; 220/2; 543/3; 574/3; 903/2; 1056/1; 1115/3; 1178/3; 1265/
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology C;Keywords: ATP; duplication; nucleotide binding; P-loop; transmembrane protein
C;Superfamily: unassigned ATP-binding cassette homology AABC1>
F;648-181/Domain: ATP-binding cassette homology AABC1>
F;649-652/Region: nucleotide-binding motif A (P-loop)
F;764-769/Region: nucleotide-binding motif A (P-loop)
F;1474-1481/Region: nucleotide-binding motif A (P-loop)
F;1586-1591/Region: nucleotide-binding motif B
                   S-adenosylmethionine-tRNA ribosyltransferase-isomerase (EC 5.4.99.-) queA PA3824 C;SpecLes: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: A83170 R;Stover;C:K:; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, A adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, F.; Lory, S.; Olson, M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Description: catalyzes the formation of dihydrodipicolinate from L-aspartate A;Pathway: lysine biosynthesis
A;Pathway: lysine biosynthesis
A;Note: first step diaminopimelate and lysine biosynthesis; sensitive to lys C;Superfamily: dihydrodipicolinate synthase
C;Keywords: carbon-oxygen lyase; hydro-lyase; lysine biosynthesis
F;171/Active site: Lys (covalent pyruvate-binding) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Go; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holr Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A; A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A; Reference number: A70500; MUID:98295987; PMID:9634230
A; Accession: H70879
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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A; Residues: 1-300 <COL>
A; Cross-references: GB.AL008967; GB:AL123456;
A; Experimental source: strain H37Rv
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75.0%;
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63.6%;
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Pred. No.
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R;Bredenbeek, P.J.; Pachuk, C.J.; Noten, A.F.H.; Charite, J.; Luytjes, W.; Weiss, Nucleic Acids Res. 18, 1825-1832, 1990
A;Title: The primary structure and expression of the second open reading frame of frameshifting mechanism.
                                                                                                                                                                                                                                                                                                                               genome polyprotein - murine hepatitis virus (strain A59)
N;Alternate names: protein 1b
N;Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-393 <SCH>
A;Cross-references: GB:S81598; NID:g1478378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Schauwecker, F.; Wanner, G.; Kahmann, R.
Biol. Chem. Hoppe-Seyler 376, 617-625, 1995
A;Title: Filament-specific expression of a cellulase gene
A;Reference number: S59499; MUID:96145728; PMID:8590631
A;Accession: S59499
A;Status: preliminary; not compared with conceptual transl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cellulase egl1 - smut fungus (Ustilago maydis)
C;Species: Ustilago maydis (corn smut)
C;Date: 20-Jul-1996 #sequence_revision 13-Mar-
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C;Superfamily: Esche
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                                                                            C; Keywords: nucleotidyltransferase;
                                                                                           A;Cross-references: EMBL:x51939; NID:g58974; PID:g1334829 C;Superfamily: infectious bronchitis virus RNA-directed R
                                                                                                                               A; Molecule type: genomic A; Residues: 1-2733 <BRE>
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C;Accession: S15760; S08652
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R; Schauwecker, F.; 1
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C; Genetics:
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A; Residues: 1-347 <STO>
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                                                                                                                                                                                                                                                                                                                C; Species: murine hepatitis virus, MHV
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   Score 39; DB Pred. No. 3.4e 2; Mismatches
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A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85905
A;Status: preliminary
                                                                                              A85905
Aypothetical protein yfiQ [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: A85905
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mau, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apo Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:AP001513; GB:BA000004; NID:g10174345; PIDN:BAB05649.1; GSPDB:GN00A;Experimental source: strain C-125 C;Genetics: A;Gene: aprX
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B83891
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A; Residues: 1-348 <HAY>
A; Cross-references: GB:BA000007; PIDN:BAB36874.1; PID:g13362922; GSPDB:GN00154
A; Experimental source: strain O157:H7, substrain RIMD 0509952
C; GenetLcs:
A; Gene: ECs3451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 28, 4317-4331, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium A; Reference number: A83650; MUID: 20512582; PMID: 11058132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: C91060
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C;Accession: C91060
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A; Residues: 1-444 <STO>
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gasawara, N.; Yasunaga, T.; Kuhara,
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Search completed: March 18, Job time: 16.5 secs

2003, 08:31:51

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Nature 413, 848-852, 2001

A; Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; A; Title: Complete genome sequence of a multiple drug resistant a: Deference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                        probable acyl-CoA synthetase STY2844 [imported] - Salmonella C;Speckes: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_chan
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A;Residues: 1-886 <STO>
A;Coss-references: GB:AE005174; NID:g12517006; PIDN:AAG57701.1; GSPDB:GN00145; UWGP:
A;Experimental source: strain O157:H7, substrain EDL933
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Davis, P.; Davies, R.M.; Dowd,
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EMBL; D64044; BAA10925.1; -.

EcoGene; EG14224; yfiQ.

InterPro; IPR003781; COA_binding.

InterPro; IPR000182; GCN5acetyltransf.

Pfam; PF00583; Acetyltransf; 1.

Pfam; PF00589; CoA_binding; 1.

Pfam; PF02629; CoA_binding; 1.
                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Dihydrodipicolinate synthase (EC 4.2.1.52) (DHDPS).
DAPA OR RV2753C OR MT2823 OR MTV002.18C.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.
                                                                                Bacteria; Actinobacteria; Actinobacteria (class); Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
-I- SIMILARITY: SOME, IN THE N-TERMINAL, TO SUCCINYL-COA LIGASES
-I- SIMILARITY: STRONG, TO M.JANNASCHII MJ0590.
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Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose I Mau B., Shao Y.;
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
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7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coli.
                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62.1%;
70.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB 1;
Pred. No. 12;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of Escherichia coli K-12.";
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                                                                                                               (class); Actinobacteridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
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K., Mayhew G.F.
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RESULT 4
QUEA_PSEAE
ID QUEA_PSEAE
AC Q9HXH8;
DT 15-JUN-2002
DT 15-JUN-2002
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V
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                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00701; DHDPS; 1.
PRINTS; PR00146; DHPTCSNTHASE.
PRODOM; PD001859; DHDPS; 1.
TIGREAMS; TIGR00674; dapA; 1.
PROSITE; PS00665; DHDPS_1; 1.
PROSITE; PS00666; DHDPS_2; 1.
Q9НХН8;
15-JUN-2002
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Whole genome comparison of Mycobacterium tuberculosis clinical laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: L-aspartate 4-semialdehyde + pyruvate = dihydrodipicolinate + 2 H(2)0.
-!- PATHWAY: BIOSYNPHESIS OF DIAMINOPIMELATE AND LYSINE FROM ASP SEMIALDEHYDE; FIRST STEP.
-!- SUBULT: HOMOTETRAMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE DHDPS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98295987; pubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Bavies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL008967; CAA15549.1; -.
EMBL; AE007110; AAK47142.1; -.
HSSP; P05640; 1DHP.
TIGR; MT2823; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva Delcheir A., Utterback T., Weidman J., Khouri H., Gricheir A.
                                                                                                                                                                                                                                                                                                    Complete proteome. ACT_SITE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TubercuList; Rv2753c; -.
InterPro; IPR002220; DHDPS.
InterPro; IPR005263; DapA.
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                                                                                                                                          VTPFSGDG
                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                    300 AA;
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                                                      STANDARD;
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                                                                                                                                                                                                                                 59.1%;
75.0%;
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Pred.
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                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                Length 300;
                                                                                                                                                                                                                                                                                    CRC64;
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                                                                                                                                                                                                               Gaps
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(Rel.

41, Created)
41, Last sequence update)

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RESULT
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                                                                                                                                                                                                                                                                                          GUNI_USTMA STANDARD; PRT; 393 AA. p54424; 01-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) Endoglucanase 1 precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase 1) (EG 1).
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STRAIN-ATCC 15692 / PAO1;

MEDLINE-20437337; PubMed-10984043;

MEDLINE-204437337; PubMed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

Garber R.L., Goltry L., Tolentino E., Westbrock Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

Opportunistic pathogen.";

Nature 406.030436473000
                                                                                                                                                         Ustilago maydis (Smut
Eukaryota; Fungi; Basi
Ustilaginomycetidae; U
UBI_TaxID=5270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Last annotation update)
S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 5.-.-.)
Schauwecker F., Wan
"Filament-specific
                         MEDLINE=96145728; PubMed=8590631; Schauwecker F., Wanner G., Kahman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                   STRAIN-FBD11
                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 406:959-964(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             272
                                                                                                                                                                                                                    Basidiomycota;
nner G., Kahmann R.;
expression of a cellulase
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Pred. No.
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2; Mismatches
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48ECBF074C2BC589
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step. The ribosyl moiety
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9.9;
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in the dimorphic
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                                                                                                                                                                                                                                                                                                                                                   RRPB_CVMA5
P16342;
01-AUG-1990
01-AUG-1990
30-MAY-2000
                                                                   "The primary structure and expression of the second open reading frame of the polymerase gene of the coronavirus MHV-A59; a highly conserved polymerase is expressed by an efficient ribosomal frameshifting mechanism.";

Nucleic Acids Res. 18:1825-1832(1990).

-I-FUNCTION: THE RNA DEPENDENT RNA POLYMERASE OF CORONAVIRUSES:
A MULTIFUNCTIONAL PROTEIN: IT CONTAINS THE ACTIVITIES NECESS:
FOR THE TRANSCRIPTION OF NEGATIVE STRANDED RNA, LEADER RNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol.
                -
                                       SUBGENOMIC MRNAS AND PROGENY VIRION RNA.
-!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate
                                                                                                                                                                                       Bredenbeek P.J., Pachuk C.J., Noten A.F.H., Charite J., Weiss S.R., Spaan W.J.M.;
                                                                                                                                                                                                                                                                              Viruses; ssRNA positive-strand Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                             CVMA5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cellulose degradation; Hydrolase; Glycosidase; Signal; Glycoprotein.
SIGNAL 1 26 POTENTIAL.
CHAIN 27 393 ENDOGLUCANASE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000334; GH_45.

Pfam; PF02015; Glyco_hydro_45; 1.

PROSITE; PS01140; GLYCOSYL_HYDROL_F45; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      movelites and this statement is not removed. Usage by and for commercial entitites requires a license agreement (See http://www.isb-sib.ch/announce/or agnd an omesi to license agreement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- TISSUE SPECIFICITY: HYPHAL TIP.
-i- DEVELOPMENTAL STAGE: EXPRESSED IN
-i- PTM: MAY ALSO BE O-GLYCOSYLATED.
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                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=90245573;
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                                                                                                                                                                                                                                                               NCBI_TaxID=11142;
                                                                                                                                                                                                                                                                                                          Murine coronavirus MHV (strain
                                                                                                                                                                                                                                                                                                                                       RNA-directed
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MISCELLANEOUS:

    Chem. Hoppe-Seyler 376:617-625(1995).
    CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic

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7; Conserv
                                                                                                                                                                                                                                                                                                                               (Rel. 15, Created)
(Rel. 15, Last sequence update)
(Rel. 39, Last annotation update)
d RNA polymerase (EC 2.7.7.48) (ORF1B).
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             THIS PROTEIN MAY BE TRANSLATED AS A 1A-1B
A RIBOSOMAL
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institutions as long as its content
atement is not removed. Usage by an
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PROTON DONOR (BY SIMILARITY)
ALA/GLY/SER-RICH.
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                                                                      OF CORONAVIRUSES IS ACTIVITIES NECESSARY RNA, LEADER RNA,
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Best Local S
Matches
                                    between
                                                                                                                                     "Ferrous active site of isopenicillin N synthase: genetic and sequenanalysis of the endogenous ligands.";
Biochemistry 35:1981-1987(1996)
-I- FUNCTION: REMOVES, IN THE PRESENCE OF OXYGEN, 4 HYDROGEN ATOMS FROM DELTA-L-(ALPHA-AMINOADLPYL)-L-CYSTEINYL-D-VALINE (ACV) TO FORM THE AZETIDINONE AND THIAZOLIDINE RINGS OF ISOPENICILLIN.
-I- COFACTOR: IRON AND ASCORBATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Isopenicillin N synthetase (EC 1.----) (IPNS)
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the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for com
entities requires a license agreement (See http://www.isb-sib.ch/an
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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NCBI_TaxID=1945;
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                                    Ween the Swiss Institute of Bioinf European Bioinformatics Institute.
                                                                                      SIMILARITY: BELCONIDOREDUCTASES.
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$15760; $15760.
$ferase; RNA-directed
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non-profit institutions as long and this statement is not removed. requires a license agreement (See
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P12851;
01-OCT-1989 (Rel.
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15-JUN-2002 (Rel.
[4]
X-RAY CRYSTALLOGRAPHY (4.1 ANGSTROMS).
MEDLINE-99190841; PubMed=10089406;
Ramin M., Shepard W., Fourme R., Kahn R.;
"Multiwavelength anomalous solvent contrast (MASC):
"Multiwavelength anomalous solvent contrast (MASC):
                                                                                                                                  missouriensis. 1. Crystallography and sit metal binding sites.";
Biochemistrumana.
                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
MEDLLINE=92304915; PubMed=1610791;
Jenkins J., Janin J., Rey F., Chiadmi M.,
Lasters I., de Maeyer M., van Belle D., Wastanssens P., Mrabet N.T., Snauwaert J., 1
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=89184498; PubMed=32377; Rey F., Jenkins J., Janin J., 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Actinoplanes missouriensis.
Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Micromonosporineae; Micromonosporaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                    Matthyssens G., Wodak S.J.;
"Structural analysis of the 2.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=90016811; PubMed=2798103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-DSM 43046;
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Pro; IPR002283; IPN_Synth.
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somerase from Actinoplanes missouriensis:
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Wodak S.J., Lauv
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PDB; 1XIN; 15-JUL-93.
PDB; 2XIN; 15-JUL-93.
PDB; 3XIN; 15-JUL-93.
PDB; 5XIN; 15-APR-93.
PDB; 1XIM; 15-APR-93.
PDB; 3XIM; 15-APR-93.
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PDB; 5XIM; 15-JUL-93.
PDB; 6XIM; 15-JUL-93.
PDB; 7XIM; 15-JUL-93.
PDB; 8XIM; 15-JUL-93.
PDB; 8XIM; 15-JUL-93.
PDB; 8XIM; 15-JUL-93.
PDB; 1BHW; 18-NOV-98.
InterPro; IPR00198; Xylose_is.
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PRINTS; PR00688
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PROSITE; PS0017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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site.";
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"Protein engineering of xylose (glucose) isomerase from Actinoplanes missouriensis. 2. Site-directed mutagenesis of the xylose binding
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[6]
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[5]
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                                                                                                                                                                                                                                    Xylose_isom; 1.8; XYLOSISMRASE.
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XYLOSE_ISOMERASE_2; 1.
e shunt; Xylose metabolism;
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de Maeyer M.,
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31, Last sequence update)
40, Last annotation update)
protein kinase (EC 2.7.1.-)
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InterPro: IPR002290; Ser_thr_pkinase.
Pfam; PP000069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG_PROSITE; PS001101; PROTEIN_KINASE_T; 1.
PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L221
InterPro;
                                                                                                      Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"The Marek's disease virus (MDV) unique short region:
"The Marek's disease virus (MDV) unique short region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sequence determination and genetic content fragment in the short unique region and the of Marek's disease virus type 1 DNA.";
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Marek's disease herpesvirus (strain GA) (MDHV).
Viruses; disease herpesvirus (strain GA) (MDHV).
Alphaherpesvirinae; Marek's disease-like viruses.
  MEDLINE=92090720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Virology 206:324-338(1995).
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                              SEQUENCE FROM N.A.
                                                                             NCBI_TaxID=4932;
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nes 6; Conserv
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110 118 ATP (BY SIMILARITY).
127 127 ATP (BY SIMILARITY).
218 218 BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X61208; CAA43522.1; --
EMBL; X63112; CAA44825.1; --
EMBL; X95720; CAA65038.1; --
EMBL; Z75259; CAA99680.1; --
PIR; A41637; A41637.
PIR; S10065; S19065.
PIR; S20174; S20174.
HSSP; Q63450; 1A06.
SGD; S0005878; MEK1
                                                                                                         NP_BIND
BINDING
ACT_SITE
                                                                                                                                                                                                                                  ProDom; PD000001; Euk_pkinase; 1.

SMART; SM00220; FHA; 1.

SMART; SM00220; FYA; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS50016; FHA_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use
                                                                                     SEQUENCE
                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00069; pkinase; 1. Pfam; PF00498; FHA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Purnelle B., Goffeau A.;
"Nucleotide sequence analysis of a 40 kb segment on the right arm
yeast chromosome XV reveals 18 open reading frames including a new
pyruvate kinase and three homologues to chromosome I genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A melosis-specific protein kinase synapsis and recombination.";
Genes Dev. 5:2392-2404(1991).
                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- CATALYTIC ACTIVITY: ATP + a protein = ADP
-i- SIMILARITY: BELONGS TO THE SER/THR FAMILY
-i- SIMILARITY: CONTAINS 1 FHA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The MRE4 gene encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000719; Euk_pkinase.
InterPro; IPR00253; FHA_domain.
InterPro; IPR002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reast 12:1475-1481(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97103776;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECOMBINATION.
Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        non-profit institutions as long as its content and this statement is not removed. Usage by ar requires a licence and removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acids Res. 20:449-457(1992).
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  Conservative
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162
168
199
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56849
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                    56.1%;
87.5%;
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o the EMBL/GenBank/DDBJ
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Saccharomyces
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0;
                    Score 37; Pred. No.
                                                                                                         ВΥ
                                                                                                                           PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                              FHA.
                                                                                  SIMILARITY.
7E197338881EF6D0 CRC64;
  Mismatches
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35;
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cerevisiae.";
                                          1:
                                                                                                                                                                                                                ATP-binding; Meiosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         + a phosphoprotein OF PROTEIN KINASES.
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                                        Length 497
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Indels
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Gaps
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EMBL; X69166; CAA48916.1; -.
EMBL; M88472; AAC34200.1; -.
EMBL; M20408; AAA28521.1; -.
PIR; S28818; S28818.
HSSP; P14921; 2STT.
FlyBase; FBgn0003118; pnt.
                                                                         InterPro; IPR000418; Ets.
InterPro; IPR002341; HSF_ETS.
Pfam; PF00178; Ets; 1.
PRINTS: DDAGGE
                                                                                                                                                                                                                                                                    entities
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pribyl L.J. Watson D.K., McWilliams M.J., Ascione R., Papas Pribyl L.J. Watson D.K., McWilliams M.J., Ascione R., Papas The Drosophila ets-2 gene: molecular structure, chromosomal localization, and developmental expression.";

Dev. Biol. 127:45-53(1988).

-i- FUNCTION: REQUIRED FOR GLIAL-NEURONAL CELL INTERACTIONS VENTRAL MIDLINE WHICH ARE NECESSARY FOR THE PROPER ELABOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PNT1_DROME STANDARD; PRT; 623 AA.
PS1022; P19420;
01-NOV-1990 (Rel. 16, Created)
10-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
ETS-11ke protein pointed P1 (D-ETS-2).
PNT OR ETSSBAB OR ETS2 OR CG17077.
DNT OR ETSSBAB OR ETS2 OR CG17077.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilia.
MCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92249640; PubMed=1577186; Chen T., Bunting M., Karim F.D., Thu "Isolation and characterization of f an ets-related DNA binding domain."; Dev. Biol. 151:176-191(1992).
                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                              :
PROSITE; PS00345; ETS_DOMAIN_1; PROSITE; PS00346; ETS_DOMAIN_2; PROSITE; PS50061; ETS_DOMAIN_3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., MEDLINE=94038653; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=88196618; PubMed=283.4248;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                     COMMISSURES IN THE EMBRYONIC CNS.
SUBCELLULAR LOCATION: Nuclear (Potential).
ALTERNATIVE PRODUCTS: 2 ISOFORMS; P1 (SHOWN HERE) AND P2 (AC P51023); ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EXPRESSED IN A COMPLEX DYNAMIC PATTERN IN EARLY EMBRYOS, INCLUDING THE MIDLINE AND MIDLINE GLIAL CELLS.
DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT DEVELOPMENT WITH LOWER LEVELS DURING LARVAL DEVELOPMENT.
SIMILARITY: BELONGS TO THE ETS FAMILY.
                                                       SM00413;
                                                                                                                                                                                                                                                                   s requires a license agreement (S
an email to license@isb-sib.ch).
                                                                     PR00454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the development of 117:163-176(1993).
                                                       ETS; 1.
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                                                                     ETSDOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pointed encodes two ETS-like proteins which are
lopment of the midline glial cells.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     five Drosophila genes that encode
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECIFICITY,
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                                                                                                                                                                                                                                                                                                      Usage
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Best Local
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Q07441;
Q1-QCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA_BIND
CONFLICT
SEQUENCE
                                                                                                       the
                                                                                                                                                                                                                                          alternative polyadenylation sites."; Gene 133:307-308(1993).
                                                             use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                     Shoji M., Hayzer D.J., Kim T.M., Runge M.S., "Human and baboon integrin beta 5 subunit-en
                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Integrin beta-5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAPCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
                              EMBL; L12231; AAA16866.1; HSSP; P05106; 1JV2.
                                                                                                                           This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                             <del>'</del>
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                                                                                                                                                                                                                                                                                                                                    Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                    between
                                                                                                                                                                                                                                                                                        MEDLINE=94040831; PubMed=8224922;
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9556;
                                                                                                                                                                                                                                                                                                                                                                   Papio cynocephalus (Yellow baboon).
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                                                                                                      ween the Swiss Institute of Bioinformatics European Bioinformatics Institute. There
                                                                                                                                                 SIMILARITY: BELONGS TO THE INTEGRIN BETA SIMILARITY: CONTAINS 1 VWFA-LIKE DOMAIN.
                                                                                                                                                                               FUNCTION: INTEGRIN ALPHA-V/BETA-5 IS A RECEPTOR FOR FIBRONEC
IT RECOGNIZES THE SEQUENCE R-G-D IT ITS LIGAND.
SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-5
ASSOCIATES WITH ALPHA-V.
SUBCELLULAR LOCATION: Type I membrane protein.
PTM: THE CYSTEINE RESIDUES ARE INVOLVED IN INTRACHAIN DISULI
                                                                                                                                                                        BONDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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66.7%;
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POLY-GLN.
POLY-THR.
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POLY-GLN.
POLY-ASN.
POLY-ASN.
POLY-ASN.
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                                                                                                                                                                                                                           IS A RECEPTOR FOR FIBRONECTIN.
IT ITS LIGAND.
                                                                                                                                                                                                                                                                                                                                                                                                                                             655
                                                                     (See http://www.isb-sib.ch/announce/
                                                                                                    There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                             A
                                                                                             as its content
                                                                                 Usage
                                                                                                                                                            CHAIN FAMILY
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                                                                                                                                                                                 INTRACHAIN DISULFIDE
                                                                                                                 and the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                   уd
                                                                                                      he EMBL outstation restrictions on it
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                                                                                                                  a collaboration
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InterPro; InterPro;

IPR000561; IPR002369; IPR001169;

EGF-like. Integrin\_B. Integrin\_beta\_C

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RESULT YOLZ CA A ID ZOA A ID ZA I
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SMART; SM00187; INB; 1.
SMART; SM00187; INB; 1.
SMART; SM00327; VWA; 1.
PROSITE; PS00243; INTEGRIN_BETA;
PROSITE; PS00022; FGF 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                           Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAEEL
YO12_0
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REPEAT
CARBOHYD
                                                                                         "2.2 Mb of contiguous nucleotide sequence elegans.";
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                          STRAIN-Bristol N2;
MEDLINE-94150718; PubMed-7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P34668;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last seg
15-JUN-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DOMAIN
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PROSITE; PS00022; EGF_1; UNKNOWN_2.
PROSITE; PS01186; EGF_2; UNKNOWN_2.
Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein; Repeat; Extracellular matrix; Cytoskeleton.
   This
                                      -!- SIMILARITY:
                                                                            Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Rhabditidae; Pelode
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Caenorhabditis elegans
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Pfam; PF00362; integrin_B;
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                                                       FUNCTION:
   SWISS-PROT
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87.5%;
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e ZK686.2 in
 ij
                                      BOX HELICASE FAMILY.
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47;
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                                                         HELICASE
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RESULT 14

RESULT 14

KKOR_YEAST

ID KKOR_Y

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P36004;
O1-JUN-1994 (Rel. 2
O1-JUN-1994 (Rel. 2
16-OCT-2001 (Rel. 4
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Pfam; PF00270; I
Pfam; PF00271; I
                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR001410; DEAD.
InterPro; IPR000629; DEAD_box.
InterPro; IPR001650; Helicase_C.
                                                                                                                                                                                                                                                                          EMBL; Z26878; CAA81519.1; EMBL; Z28168; CAA82010.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94378719; PubMed=8091858; Vandenbol M., Bolle P.-A., Dion C., "Sequencing and analysis of a 20.5 arm of yeast chromosome XI."; Yeast 10:525-533(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinformatics and the E
the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomycetales;
NCBI_TaxID=4932;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Probable serine/threonine-protein YKL168C OR YKL632.
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Hypothetical protein; Helicase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S44912; S44912.
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helicase_C; 1.
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380 D
78376 MW;
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InterPro; IPR000719; Euk\_pkinase. InterPro; IPR002290; Ser\_thr\_pkinase.

YKL168C

PF00069;

pkinase;

PD000001;

; S37998; S37998. ; S38413; S38413. ; S44593; S44593; ; S0001651; YKL1680

SQ

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RA Feng X., Teitelbaum S.L., Quiroz M.E., Towler D.A., Ross F.P.;
RT "Cloning of the murine beta5 integrin subunit promoter. Identification RT of a novel sequence mediating granulocyte-macrophage colony-
RT stimulating factor-dependent repression of beta5 integrin gene
RT stimulating factor-dependent repression of beta5 integrin gene
RT J. Biol. Chem. 274:1366-1374(1999).
RL J. Biol. Chem. 274:1366-1374(1999).
CC IT RECOGNIZES THE SEQUENCE R-G-D IT ITS LIGAND.
CC IT RECOGNIZES THE SEQUENCE R-G-D IT ITS LIGAND.
CC IT RECOGNIZES THE SEQUENCE R-G-D IT ITS LIGAND.
CC IT SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-5
CC ASSOCIATES WITH ALPHA-V.
CC ASSOCIATES WITH ALPHA-V.
CC ISUBCELLULAR LOCATION: Type I membrane protein.
CC ISUBCELLULAR ENCOUCTS: TROPONKS; BETA-5A (SHOWN HERE) AND BETA-
CC SUBCELLULAR SELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
CC ISIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
CC ISIMILARITY: CONTAINS 1 YWFA-LIKE DOMAIN.
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ATP-binding, 422 722
DOMAIN 428 436
BINDING 458 465
ACT_SITE 573 573
SEQUENCE 734 AA; 836
                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                070309; 070308; 088347;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Integrin beta-5 precursor.
                                                                                                    use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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ITB5_MOUSE
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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      ; AF043257; AAC40110.
; AF043256; AAC40109.
; AF022110; AAD08782.
; P05106; 1JV2.
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PS50011;
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InterPro; IPR002369; Integrin_B.
InterPro; IPR001369; Integrin_beta_C.
InterPro; IPR003659; Plexin-like.
InterPro; IPR002035; VWF_A.
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SM00187; INB;
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SM00327; VWA;
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ERSRAYYEMAS.NPLYRKPISTHTVDFAFNKSYNGSV-> LKPPYOKAHLHTHCRFTLQOVQOILQWLSGLRLLOGWRGTKDEDSGVPWTSWTICSR (IN ISOFORM BETA-5B).

S-> C (IN REF. 2).

K -> R (IN REF. 2).

K -> R (IN REF. 2).

MW; 34B9DBBO7F^^^
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    56.1%;
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EXTRACELLULAR (1
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Length 798;
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RESULT ITB5\_M

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Best Local Similarity 87.5%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DNDISPFS 8
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Db 184 DKDISPFS 191

Search completed: March 18, 2003, 08:30:14

Job time: 10.5 secs

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Result
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Q924I1
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            Q9J3F2
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O9nq76 homo sapien
Q95kg5 macaca fasc
O9gml3 macaca fasc
O9n076 macaca fasc
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O9n076 rattus musculu
O9es02 rattus norv
O9pq03 ureaplasma
O9y819 schizosacch
O8yzq1 anabaena sp
O8yzq1 anurine hepa
O9bya2 murine hepa
O9bya2 murine hepa
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O8vik4 mus musculu
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| 45     | 44     | 43                 | 42                 | 41                 | 40     | 39     | 38     | 37                | 36     | <u>ა</u> | 34     | 33              | 32                | 31     | 30     | 29                 | 28     | 27                 | 26                 | 25     | 24     | 23     | 22     | 21       | 20     | 19     | 18     | 17                 |
|--------|--------|--------------------|--------------------|--------------------|--------|--------|--------|-------------------|--------|----------|--------|-----------------|-------------------|--------|--------|--------------------|--------|--------------------|--------------------|--------|--------|--------|--------|----------|--------|--------|--------|--------------------|
| 37     | 37     | 37                 | 37                 | 37                 | 37     | 37     | 37     | 37                | 37     | 37       | 38     | 38              | 38                | 38     | 38     | 38                 | 38     | 38                 | 38                 | 38     | 38     | 38     | 38     | 38.5     | 39     | 39     | 39     | 39                 |
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| 640    | 542    | 501                | 500                | 500                | 490    | 402    | 389    | 370               | 354    | 233      | 1967   | 886             | 886               | 886    | 736    | 673                | 546    | 480                | 459                | 444    | 348    | 338    | 104    | 793      | 2733   | 2733   | 466    | 434                |
| 16     | 10     | 10                 | 11                 | 11                 | 17     | 12     | S      | G                 | Ν      | 10       | 12     | 16              | 16                | 16     | 10     | 10                 | N      | 10                 | 11                 | 16     | 16     | 10     | 10     | ഗ        | 12     | 12     |        |                    |
| Q9CKM9 | Q9SV40 | Q93Z04             | Q91ZV7             | Q9CWV5             | 027541 | Q9E6L8 | Q9N5B5 | Q9VX05            | Q9L6W9 | 048898   | 010378 | Q8 <b>X</b> 9F6 | Q8Z4J4            | Q8ZMX2 | Q9AY58 | Q94GI5             | Q8RNY5 | Q9XE29             | Q9D852             | 09квл7 | Q8X2E2 | Q9FKN7 | Q9LGC8 | Q9VVY0   | Q9J3E8 | 039226 | 093785 | Q9P456             |
|        | _      | Q93z04 arabidopsis | Q91zv7 mus musculu | Q9cwv5 mus musculu |        | 8      |        | Q9vx05 drosophila | 7      | agro     |        | esch            | Q8z4j4 salmonella | salmo  |        | Q94gi5 oryza sativ |        | Q9xe29 oryza sativ | Q9d852 mus musculu |        |        |        | В      | drosophi | murine | 6      |        | Q9p456 aspergillus |

## ALIGNMENTS

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RESULT 1
Q9NQ76
ID Q9NQ
AC Q9NQ
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Query Match
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Matches 12; Conserv
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Q9NQ76;
Q1-CCT-2000 (TrEMBLrel. 15, Created)
O1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Matrix extracellular phosphoglycoprotein precursor.
                                                                                                                                           CHAIN
SEQUENCE
                                                                                                                                                                                                            Signal.
SIGNAL
                                                                                                                                                                                                                                                                     Argiro L., Desbarats M., Glorieux F.H., Ecarot B.;
"Mepe, the gene encoding a tumor-secreted protein in oncogenic hypophosphatemic osteomalacia, is expressed in bone.";
Genomics 74.342-551(2001).
EMBL; AJ276396; CAB97250.1;
EMBL; AF325916; AAK70343.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "MEPE, a new gene expressed in bone marrow and tumors causing osteomalacia."; Genomics 67:54-68(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=21309068; PubMed=11414762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20399567; PubMed=10945470; Rowe P.S.N., De Zoysa P.A., Dong R., Econs M.J., Oudet C.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=BONE;
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100.0%; ilarity 100.0%; Conservative (
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58419 MW;
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MATRIX EXTRACELLULAR PHOSPHOGLYCOPROTEIN.

0977CA6E871CA9E5 CRC64;
Score 66; DB 4;
Pred. No. 0.00072;
Mismatches 0;
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                                                                    Length 525;
   Indels
   0
   Gaps
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Q95KG5;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Mypothetical 55.6 kDa protein.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                  Q9GM13;
Q9GM13;
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
                                                                                                libraries.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases EMBL; AB050259; BAB17010.1; -. PDAD47E88038A9E2 CRC64;
                                                                                                                                                Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Suzuki Y., Sugano S., Hashimoto K.; Suzuki Y., Sugano S., Hashimoto K.; "Isolation of full-length cDNA clones from macaque brain cDNA".
                                                                                                                                                                                                                                                   Macaca fascicularis (Crab eating macaque) (Cynomolgus monk
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-TEMPORAL LOBE RIGHT;
OSAda N., Hida M., Kusuda J., Tanuma F
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones
                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE-BRAIN PARIETAL LOBE;
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Submitted (APR-2001) to the
EMBL; AB060891; BAB46894.1;
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280
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DNDMSPFSGDGQ
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                                                           Similarity
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91.7%;
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91.7%;
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Last annotation updat
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Pred. No.
                                               Pred. No. 0.0028;
l; Mismatches
                                                                        Score 63;
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Q9ES02;
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SIGNAL
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EMBL; AF314964; AAK70342.1; ...
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Q9N076; O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             092411;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Osada N., Hida M., Kusuda J., Tanuma R., Iseki Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from mac libraries.",
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ EMBL, AB046056; BAB01638.1;
SEQUENCE 555 AA; 61979 MW; CCFE1A9BADA19EB
                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J;
MEDLINE=21309068; PubMed=11414762;
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Mammalia; Eutheria;
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Macaca fascicularis (Crab eating macacque) (Cynomolgus monkey).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:2137384; Mepe.
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                                                                                                                                               177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Argiro L., Desbarats M., Glorieux F.H., Ecarot B., "Mepe, the gene encoding a tumor-secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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433 AA;
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Rodentia;
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MATRIX EXTRACELLULAR PHOSPHOGLYCOPROTEIN.

7CD603CAA8CB41B0 CRC64;
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Pred. No. 0.
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STRAIN-SEROVAR 3;
MEDLINE-20500219; PubMed-11048724;
The Lefkowitz E.J., Glass J.S.,
               Q9Y819;
01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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J. Biol. Chem. 275:36172-36180(2000).
EMBL, AF260922; AAG33366.1;
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MEDLINE-20549633; PubMed-10967096;
Petersen D.N., Tkalcevic G.T., Man
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01-MAR-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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Mammalia; Eutheria;
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Rattus norvegicus (Rat).
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Q8VA07;
Q1-MAR-2002
Q1-MAR-2002
Q1-JUN-2002
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01-MAR-2002
01-MAR-2002
01-MAR-2002
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Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watanabe A., Iriguchi M., Ishikwa A., Kawashima K., Kimura T.
Watanabe A., Iriguchi M., Ishikwa A., Kawashima K., Kimura T.
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.;
"Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
EMBL; AP003882; BAB72364.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPBC1105.08.
Schizosaccharomyces pombe (Fission yeast).
Schizosaccharomycetes;
  Nonstructural protein 1
Chikungunya virus.
Viruses; ssRNA positive
                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical SEQUENCE 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anabaena sp. (strain PCC Bacteria; Cyanobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8YZQ1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-1999) to the EMBL; AL096851; CAB50971.1; InterPro; IPR004240; EMP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McDougall R.C., R
Bothe G., Pohl T;
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8; Conserv
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2 (TrEMBLrel.
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420 AA; 4
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(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
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  positive-strand viruses,
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DNA stage;
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  Togaviridae;
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Q8XRZ9;
01-MAR-2002 (TIEMBLIEL .
01-MAR-2002 (TIEMBLIEL .
01-JUN-2002 (TIEMBLIEL .
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Q9J3F2;
Q1-OCT-2000 (
01-OCT-2000 (
01-DEC-2001 (
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EMBL; AL646080; CAb17833.1; ...
InterPro: IPR000205; NAD_binding.
InterPro: IPR001155; Oxidored_FMN.
Pfam; PF00724; Oxidored_FMN; IOXIdored_FMN; Complete proteome.
Oxidoreductase; Plasmid; Complete proteome.
SEQUENCE 726 AA; 79888 MW; 667F300EE32805DC
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Submitted (OCT-2001) to the EMBL/Gen
EMBL; AF438162; AAL30897.1; -
InterPro; IPR002588; V_methyltransf.
Pfam; PF01660; Vmethyltransf; 1.
NON_TER 536 536
RNA-directed
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Siguier P., Thebault P., Whalen M.,
Weissenbach J., Boucher C.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probable trimethylamine (EC 1.5.99.-).
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RSP0682 OR RS01767.
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20, Last sequence update)
21, Last annotation update)
dehydrogenase oxidoreductase
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Pred. No.
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                  RESULT
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AC Q0
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Q90W20;
01-DEC-2001
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RESULT 13
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Best Local
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STRAIN-PENN 97-1;

Das Sarma J., Hingley S.T., Lai M.M.C., Weiss S.R., L

*Pathogenesis and sequence analysis of mouse hepatiti

*Pathogenesis and sequence of acute meningitis and
                                                                                                                                                                                                                                                                            Submitted [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9PYA2
Q9PYA2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; ssRNA positive-strand Coronaviridae; Coronavirus. NCBI_TaxID=11138;
2531
                                                                                                                                                                                                                                                                                                                   STRAIN=MHV-2; Das Sarma J., Hingley S.T., Lai M.M.C., Weiss S.R., Lavi E.; Pathogenesis and sequence analysis of mouse hepatitis virus ty an experimental model system of acute meningitis and hepatitis
                                                                                                                                                                                                                                                                                                                                                                                                                    murine hepatitis virus.
Viruses; ssRNA positive-strand
Coronaviridae; Coronavirus.
                                                                                                                RNA-directed RNA polymerase SEQUENCE 2733 AA; 309420
                                                                                                                                           EMBL; AF201929; AAF19384.1; EMBL; AF207902; AAF68920.1;
                                                                                                                                                                                           an experimental model system mice ":
                                                                                                                                                                                                   Das Sarma J., Hingley S.T., Lai M.M.C., "Pathogenesis and sequence analysis of an experimental model system of acute me
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (NOV-1999) to the EMBL; AF208066; AAF69332.1;
                                                                                                                                                                         Submitted (NOV-1999) to the
                                                                                                                                                                                       mice
                                                                                                                                                                                                                                               STRAIN-ML-
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Viruses; ssRNA positivo
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tis virus
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RESULT 15
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AC Q8VIK
AC Q8VIK
AC Q8VIK
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-UM
CG CD05
GN CD15
GN CD15
GN WGBI
RN [1]
RN [1]
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RC STMAI
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Search completed: March 18, 2003, 08:31:14 Job time : 29 secs
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Matches
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OBVIK4; PRELIMINARI,
O1-MAR-2002 (TrEMBLrel. 201-JUN-2002 (TrEMBLrel. 201-JUN-2002 (TrEMBLrel. 201-JUN-2002)
                                                                                                                                                                                                                                                                                                       Pram; Pr00059; lectin_c; 1.

SMART; SM00034; CLECT; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; UNKNOWN_1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

SEQUENCE 207 AA; 23500 MW; 16FB4EB47ECAD3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNR3.
CD209D OR SIGNR3.
Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Weltzien F.A., Kobayashi T., Andersson E., Norberg B., Andersen O.;

"Molecular characterization of FSH-beta, LH-beta, and alpha-subunit of
Atlantic halibut (Hippoglossus hippoglossus).";

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ417768; CAD10501.1; -.

InterPro; IPR000359; Cys_knot.

Pfam; PF00007; Cys_knot; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Park C.G., Steinman R.M.;

"Alternatively Spliced Forms of Mouse DC-SIGN Homologs.";

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF440280; AAL33584-1; -.

MGD; MGI:2157947; CD209d.

InterPro; IPR001304; Lectin_C.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Meopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;

Acanthomorpha; Houronectidae; Hippoglossus.
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6;
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Last annotation update)
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                                                                                                                                                                                                                                     Score 39; DB Pred. No. 28;
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290CEE379861A34F CRC64;
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                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to hav score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.
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39
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Maximum Match 100%
Listing first 45 summaries
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1988 DAT: *
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990 DAT: *
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1991 DAT: *
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1992 DAT: *
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1993 DAT: *
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
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AAO203737
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AAO20353
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49.200 Million cell updates/sec
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| 45                 | 44                 | 43                | 42                 | 41                 | 40                 | 39                 | 38                 | 37                 | 36                 | 35       | 34                 | 33                 | 32       | 31       | 30                 | 29                 | 28                 | 27                 | 26                 | 25                 | 24                 | 23                 | 22                 | 21                 | 20                 | 19       | 18       | 17                 | 16                 | 15  | 14       | 13       | 12    | 11               |
|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|--------------------|--------------------|----------|----------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|----------|----------|--------------------|--------------------|-----|----------|----------|-------|------------------|
| 35                 | 35                 | 35                | 35                 | 35                 | 35                 | 35                 | 35                 | 35                 | 36                 | 36       | 36                 | 36                 | 36       | 36       | 36                 | 36                 | 36                 | 36                 | 36                 | 36                 | 36                 | 36                 | 36                 | 36                 | 39                 | 39       | 39       | 39                 | 39                 | 39  | 39       | 39       | 39    | 39               |
| 89.7               | •                  | •                 |                    |                    |                    | •                  | •                  |                    |                    |          | •                  |                    |          | •        |                    | •                  | 92.3               |                    |                    |                    | •                  |                    |                    |                    |                    | •        | 100.0    | •                  | •                  | •   | •        |          | 100.0 | 100.0            |
| 531                | 450                | 432               | 384                | 384                | 368                | 367                | 336                | 47                 | 1391               | 1133     | 1104               | 1069               | 1004     | 778      | 778                | 665                | 664                | 504                | 358                | 350                | 350                | 349                | 349                | 328                | 556                | 540      | 525      | 525                | 525                | 525 | 509      | 430      | 430   | 348              |
| 21                 | 22                 | 22                | 23                 | 22                 | 21                 | 21                 | 21                 | 21                 | 21                 | 21       | 21                 | 21                 | 22       | 22       | 22                 | 21                 | 21                 | 22                 | 21                 | 21                 | 21                 | 21                 | 21                 | 22                 | 22                 | 22       | 23       | 23                 | 22                 | 22  | 22       | 22       | 21    | 20               |
| AAG24871           | AAU33718           | AAE04642          | AAU85179           | AAU24559           | AAG15423           | AAG15424           | AAG15425           | AAG57290           | AAY44644           | AAG29229 | AAG29230           | AAG29231           | AAE07164 | ABB66160 | ABB60520           | AAG29449           | AAG29450           | AAU16220           | AAG07577           | AAG50444           | AAG14087           | AAG50445           | AAG14088           | ABB64344           | AAB82921           | AAB82923 | AAE13227 | ABB08526           | 268                | 292 | AAB82922 | AAB62669 | 5381  | AAY39324         |
| Arabidopsis thalia | Pseudomonas aerugi | Bacillus subtilis | G-coupled olfactor | Human olfactory re | Arabidopsis thalia | Arabidopsis thalia | Arabidopsis thalia | Arabidopsis thalia | Candida albicans a |          | Arabidopsis thalia | Arabidopsis thalia |          |          | Drosophila melanog | Arabidopsis thalia | Arabidopsis thalia | Human novel secret | Arabidopsis thalia | Drosophila melanog | Human osteoregulin |          |          | Human phosphatonin | Phosphatonin polyp |     | ന        | ಌ        | C     | PSGen12 protein. |

# ALIGNMENTS

RESULT 1 AAO20372

31-MAY-2002 (first entry)

AAO20372;

AA020372 standard; peptide; 12 AA.

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Bone growth; RGD motif; integrin binding motif; calcium binding motif; glycosaminoglycan binding motif; bone loss; renal phosphate excretion; alveolar; teeth; odontoblast; osteoclast; dental tissue; skeletal loss
                                                                 16-AUG-2000;
19-MAR-2001;
                                                                                                                                            Unidentified.
                WPI; 2002-291971/33.
                                 Kumagai Y,
                                                 (BIGB-) BIG BEAR BIO INC
                                                                                          14-AUG-2001; 2001WO-US25542
                                                                                                            21-FEB-2002
                                                                                                                            WO200214360-A1
                                                                                                                                                              weakness.
                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                        of a
                                Blacher RW,
                                                                 2000US-0641034
2001US-0812485
                                                                                                                                                                                                       calcium binding motif
                                 Yoneda
                                 H,
                                                                                                                                                                                                         #1
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New peptide compound useful for reducing bone loss, is capable

of

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RESULT 2
AAO20373
ID AAO2
XX AAO2
XX AAO2
XX AAO2
XX AAO2
XX AAO2
XX BON
KW BON
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Best Local S
Matches 6
16-AUG-2000; 2000US-0641034
                                                                     14-AUG-2001; 2001WO-US25542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bone growth; RGD motif; integrin binding motif; calcium binding motif; glycosaminoglycan binding motif; bone loss; renal phosphate excretion; alveolar; teeth; odontoblast; osteoclast; dental tissue; skeletal loss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a peptide compound capable of enhancing bone growth, and comprising 10-50 amino acids in a sequence, where the amino acids are in D- or L- conformation and the sequence comprises a motif selected from an integrin binding motif, a glycosaminoglycan binding motif and a calcium binding motif, a glycosaminoglycan binding for reducing bone loss and for reducing renal phosphate excretion in an individual. The peptide is useful for promoting regeneration of alveolar bone and/or teeth, and increases the number and activity of odontoblasts contracts that help form dental tissues. The peptide is also useful for treating or preventing a condition associated with skeletal loss or weakness. This sequence represents a peptide of the calcium binding motif
                                                                                                                        21-FEB-2002
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Pred. No. 1
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RESULT 3
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ID AAU9
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Best Local 9
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                                                                                                                                                                                                                                                                                       Dental product; toothpaste; mouthwash; dental floss; bone growth; integrin binding motif; RGD; skeletal disease; dental disease; tooth; alveolar bone growth; osteoblast; odontoblast; osteopathic.
                                                                                                                                                                                   09-AUG-2001; 2001WO-US25101
                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                       02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptide compound useful for reducing bone loss, is capable of enhancing bone growth, and comprises an integrin binding motif, glycosaminoglycan binding motif or a calcium binding motif -
                                                                                                      Yoneda T,
                                                                                                                                                         16-AUG-2000; 2000US-225879P
                                                                                                                                                                                                             21-FEB-2002
                                                                                                                                                                                                                                       WO200213775-A1
                                                                                                                                                                                                                                                                                                                                            Dental product bone growth enhancing peptide #44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                         AAU93724 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-MAR-2001; 2001US-0812485
                                                                                                                                (BIGB-) BIG BEAR BIO INC.
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12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 AA;
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1.9;
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Claim 12; Page 21; 44pp; English

Dental product useful for treating skeletal diseases e.g. diseases comprises a base material and a compound comprise amino acid in a sequence containing the integrin binding r

sing specific motif dental

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RESULT 4
RAGOUNT 7
ID 2007
ID 
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                   The invention relates to a peptide compound capable of enhancing bone growth, and comprising 10-50 amino acids in a sequence, where the amino acids are in D- or I- conformation and the sequence comprises a motif selected from an integrin binding motif, a glycosaminoglycan binding motif and a calcium binding motif. The peptide of the invention is useful for reducing bone loss and for reducing renal phosphate excretion in an integring bone loss and for reducing renal phosphate excretion in an integring bone loss and for reducing renal phosphate excretion in an integring the sequence of the invention is useful for reducing bone loss and for reducing renal phosphate excretion in an integring the sequence.
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                                                                                                                                                                                                                                                                                                         New peptide compound useful for reducing bone loss, is capable enhancing bone growth, and comprises an integrin binding motif, glycosaminoglycan binding motif or a calcium binding motif -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bone growth; RGD motif; integrin binding motif; calcium binding motif; glycosaminoglycan binding motif; bone loss; renal phosphate excretion; alveolar; teeth; odontoblast; osteoclast; dental tissue; skeletal loss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-AUG-2000; 2000US-0641034
19-MAR-2001; 2001US-0812485
for reducing bon
                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-291971/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kumagai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-AUG-2001; 2001WO-US25542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200214360-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         weakness;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C-terminal amidated synthesised peptide D-00004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA020377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAO20377 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                      Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BIGB-) BIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bone growth enhancing peptides for use in dental products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DXDXSXFXGXXQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 DNDISPFSGDGQ 15
                                                                                                                                                                                                                                                      Page 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blacher RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BEAR BIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "C-terminal amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide;
                                                                                                                                                                                                                                            50pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INC
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                                                                                                                                                                                                                                                   English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Τ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB . 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                         g motif,
g motif -
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                                                            useful
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DXDXSXFXGXXQ

Best Matches Query Match

Local

Similarity 6; Conser

Conservative

9

Pred. No. 4; 6; Mismatches Score

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Gaps

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39; DВ

23;

Length 23;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                      and/or alveolar bone growth on areas where deterioration has occurred, as well as the growth or recruiting of osteoblast or odontoblast cells on the surface of the new skeletal growth. AA093681-AAU93726 represent
                                                                                   motif such as RGD in the D- or L- form, preferably the L-configuration The peptides of the invention are useful for treating or preventing skeletal diseases such as dental disease. The peptides enhance tooth
                                                                                                                            The present invention relates to dental products such as toothpastes, mouthwash and dental floss comprising a base material and a compound which promotes bone growth. Such compounds are peptide sequences comprising 10-50 amino acids and containing an integrin binding
                                                                                                                                                                                                                                   Dental product useful for treating skeletal diseases e.g. dental diseases comprises a base material and a compound comprising specific amino acid in a sequence containing the integrin binding motif -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bone and/or teeth, and increases the number and activity of odontoblas /osteoclasts that help form dental tissues. The peptide is also useful for treating or preventing a condition associated with skeletal loss oweakness. This sequence represents a C-terminal amidated synthesised
 Sequence
                                                                                                                                                                                                       Claim 7; Page 21; 44pp; English.
                                                                                                                                                                                                                                                                                               WPI; 2002-329525/36.
                                                                                                                                                                                                                                                                                                                                                                                                                   09-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                              21-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alveolar bone growth; osteoblast; odontoblast; osteopathic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dental product bone growth enhancing peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU93726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU93726 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                           bone growth enhancing peptides
                                                                                                                                                                                                                                                                                                                           Yoneda T,
                                                                                                                                                                                                                                                                                                                                                                                     16-AUG-2000; 2000US-225879P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200213775-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dental product; toothpaste;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide D-00004 of the invention.
                                                                                                                                                                                                                                                                                                                                                        (BIGB-) BIG BEAR BIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dental product; toothpaste; mouthwash; dental floss; bone growth;
integrin binding motif; RGD; skeletal disease; dental disease; tooth;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 DXDXSXFXGXXQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                           Nomizu M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 AA;
 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry)
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                                                                                                                                                                                                                                                                                                                                                          INC
                                                                                                                                                                                                                                                                                                                           Kumagai
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                                                                                                                                                                                                                                                                                                                           Υ;
                              for use in dental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39;
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                             products.
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DNDISPFSGDGQ

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RESULT 6
AA020379
ID AA020379
ID AA020
XX AA02
XX AA02
XX BONE
KW BONE
KW Glycc
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XX Synt
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RESULT 7
AAU93703
ID AAU9
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                                                                                                                                                                                                                                                                                                          Query Match
Best Local (
                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a peptide compound capable of enhancing bone growth, and comprising 10-50 amino acids in a sequence, where the amino acids are in D- or L- conformation and the sequence comprises a motif selected from an integrin binding motif, a glycosaminoglycan binding motif and a calcium binding motif. The peptide of the invention is useful for reducing bone loss and for reducing renal phosphate excretion in an individual. The peptide is useful for promoting regeneration of alveolar bone and/or teeth, and increases the number and activity of odontoblasts /osteoclasts that help form dental tissues. The peptide is also useful for treating or preventing a condition associated with skeletal loss or meakness. This sequence represents a C-terminal amidated synthesised contention of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New peptide compound useful for reducing bone loss, is capable of enhancing bone growth, and comprises an integrin binding motif, glycosaminoglycan binding motif or a calcium binding motif -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                            AAU93703 standard;
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide D-00006 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 15; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kumagai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-AUG-2000;
19-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bone growth; RGD motif; integrin binding motif; calcium binding motif; glycosaminoglycan binding motif; bone loss; renal phosphate excretion; alveolar; teeth; odontoblast; osteoclast; dental tissue; skeletal loss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C-terminal amidated synthesised peptide D-00006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-2001; 2001WO-US25542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            weakness;
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                                                                                                                                                                                                                           DXDXSXFXGXXQ 12
                                                                                                                                                                    DNDISPESGDGQ 19
                                                                                                                                                                                                                                                                                Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D00006
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                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Blacher
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0641034
2001US-0812485
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                                                                                                                                                                                                                                                                                                                                                                                              ΑĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                            peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide;
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                                                                                                                                                                                                                                                                                                             Score 39;
Pred. No. 4;
                            AA.
                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                    Length 23;
                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                       SXCCCCCCCCCXXXXIII
                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to dental products such as toothpastes, mouthwash and dental floss comprising a base material and a compound which promotes bone growth. Such compounds are peptide sequences comprising 10-50 amino acids and containing an integrin binding motif such as RGD in the D- or L- form, preferably the L-configuration. The peptides of the invention are useful for treating or preventing skeletal diseases such as dental disease. The peptides enhance tooth and/or alveolar bone growth on areas where deterioration has occurred, as well as the growth or recruiting of osteoblast or odontoblast cells on the surface of the new skeletal growth. AAU93861-AAU93726 represent bone growth enhancing peptides for use in dental products.
                                                                      glycosaminoglycan binding alveolar; teeth; odontoble
                             Unidentified
                                                                      Bone growth; RGD motif; integrin binding motif; calcium glycosaminoglycan binding motif; bone loss; renal phosph alveolar; teeth; odontoblast; osteoclast; dental tissue;
                                                                                                                                                                                                                  AAO20353 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dental product; toothpaste; mouthwash; dental floss; bone growth; integrin binding motif; RGD; skeletal disease; dental disease; tooth; alveolar bone growth; osteoblast; odontoblast; osteopathic.
                                                        weakness; matrix extracellular phosphoglycoprotein.
                                                                                                                             Protein of matrix extracellular phosphoglycoprotein containing
                                                                                                                                                           31-MAY-2002
                                                                                                                                                                                       AA020353;
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dental product useful for treating skeletal diseases e.g. dental diseases comprises a base material and a compound comprising specific amino acid in a sequence containing the integrin binding motif \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yoneda T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dental product bone growth enhancing peptide
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                                                                                                                                                                                                                                                                                                                                               Similarity 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                       40 AA;
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                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                    calcium binding motif;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a peptide compound capable of enhancing bone growth, and comprising 10-50 amino acids in a sequence, where the amino acids are in D- or L- conformation and the sequence comprises a motif selected from an integrin binding motif, a glycosaminoglycan binding motif and a calcium binding motif. The peptide of the invention is useful for reducing bone loss and for reducing renal phosphate excretion in an individual. The peptide is useful for promoting regeneration of alveolar bone and/or teeth, and increases the number and activity of odontoblasts osteoclasts that help form dental tissues. The peptide is also useful for treating or preventing a condition associated with skeletal loss or weakness. This sequence represents a protein of a matrix extracellular phosphoglycoprotein containing an RGD motif of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New peptide compound useful enhancing bone growth, and c glycosaminoglycan binding mc
                                                                                                                                                                                                                                                                                                                                                                                                               integrin bindi
alveolar bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dental product; toothpaste; mouthwash;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dental product bone growth enhancing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU93681 standard; protein;
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19-MAR-2001;
     WPI; 2002-329525/36
                                                     Yoneda T,
                                                                                                                                                          16-AUG-2000; 2000US-225879P
                                                                                                                                                                                                       09-AUG-2001; 2001WO-US25101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kumagai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-AUG-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conserv
                                                                                                       BIG
                                                                                                                                                                                                                                                                                                                                                                                                                                          binding motif;
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                                                  Nomizu M,
                                                                                                     BEAR BIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blacher RW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                            ing motif; RGD; skeletal disease;
growth; osteoblast; odontoblast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Æ
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                                                     Kumagai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seful for reducing bone loss, is capable and comprises an integrin binding motif, ing motif or a calcium binding motif
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                                                                                                                                                                                                                                                                                                                                                                                                                                  dental floss; bone growth; disease; dental disease; to
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                                                                                                                                                                                                                                                                                                                                                                                                            osteopathic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bone growth; RGD motif; integrin binding motif; calcium binding motif; glycosaminoglycan binding motif; bone loss; renal phosphate excretion; glycosaminoglycan binding motif; bone loss; renal phosphate excretion; alveolar; teeth; odontoblast; osteoclast; dental tissue; skeletal loss;
                                                                                                                                                                                                                    New peptide compound useful for reducing bone loss, is capable enhancing bone growth, and comprises an integrin binding motif, glycosaminoglycan binding motif or a calcium binding motif -
                                                                                                                                                                                                                                                                                                                                    WPI;
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                                                                                                                                                                   Disclosure; Page 11;
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19-MAR-2001;
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DNDISPFSGDGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              BEAR BIO INC
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                                                                                                                                                                English.
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Pred. No. 22;
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The invention relates to a peptide compound capable of enhancing bone growth, and comprising 10-50 amino acids in a sequence, where the amin acids are in D- or L- conformation and the sequence comprises a motif selected from an integrin binding motif, a glycosaminoglycan binding motif and a calcium binding motif. The peptide of the invention is usually constitution of the invention is usually constitution.

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03-NOV-1998;
23-NOV-1998;
the band pattern produced in conventional differential RNA display (where bands may be obscured, resulting in false positive signals) since most bands common to both samples are eliminated, allowing identification and cloning of genes displaying anticipated differential expression. RSDD
                                                                                                         This is the amino acid sequence of the PSGen12 protein (progression suppressed gene 12). PSGen12 has suppressed expression in progressed tumour cells. The PSGen12 nucleic acid sequence was identified using new methods for identifying nucleic acids differentially expressed between two samples. The method involves performing reciprocal subtraction differential RNA display (RSDD) between the two samples to generate two subtraction samples. The subtraction samples are amplified and compared to identify those nucleic acids that are differentially expressed genes, used to identify and clone differentially expressed genes, particularly those with increased or reduced expression during tumour particularly those with increased or reduced expression during tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for reducing bone loss and for reducing renal phosphate excretion in an individual. The peptide is useful for promoting regeneration of alveolar bone and/or teeth, and increases the number and activity of odontoblasts /osteoclasts that help form dental tissues. The peptide is also useful for treating or preventing a condition associated with skeletal loss or weakness. This sequence represents a protein of a matrix extracellular phosphoglycoprotein containing an RGD motif of the invention.
                                                                            cell progression, e.g. progression suppressed genes (PSGen) and progression elevated genes (PEGen). The method reduces the comp
                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Progression suppressed gene; PSGen; progression elevated tumour; reciprocal subtraction differential RNA display;
                                                                                                                                                                                                                                                                                                                          Identifying nucleic acids differentially expressed between two samples, particularly sequences involved in tumour progression
                                                                                                                                                                                                                                                                                                                                                                                                                        Fisher
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DB; AAZ21516.
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98US-0185115.
98US-0197889.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     only a single anchored primer for amplification and reamplified be analysed by reverse Northern blotting.
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143..148
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139..142
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199..20
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194..197
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119..2
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77..79
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Pred. No. 99;
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New polypeptides involved useful for diagnosing and
                             phosphatonin in a subject modulates Na+-dependent phosphate cotransport, vitamin D metabolism and/or bone mineralisation. The phosphatonin
                                               The present sequence represents a phosphatonin polypeptide (also called Metastatic-tumour Excreted Phosphaturic-Element (MEPE)). The level of
                                                                              Claim
                                                                                                metabolism
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04-SEP-1998;
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         polypeptides, polynucleotides, vectors and antibodies are phosphate metabolism related disease. They are used for
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98GB-0019387
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291..296
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238..241
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312..3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "myristoylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                      "protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                          "myristoylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                              "protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "protein kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "myristoylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "myristoylation
                                                                                                                                                                                                                                                                                                                                                                                         cAMP and cGMP dependent protien kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                     protein kinase C
                                                                                                       in the regulation of phosphate metabolism treating disorders related to phosphate
                   vectors and antibodies are used to
                                                                                                                                                                                                                                                                                                                                kinase II
                                                                                                                                                                                                                                                                                                                kinase
                                                                                                                                                                                                                                                                                                                                                                        kinase C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                             kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kinase C phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      site"
                                                                                                                                                                                                                                                                                                              ΪI
                                                                                                                                                                                                                                                                                                                                                                                                                                           site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          site"
                                                                                                                                                                                                                                                                                                                                 phosphorylation
                                                                                                                                                                                                                                                                                                                                                     phosphorylation
                                                                                                                                                                                                                                                                                                                                                                        phosphorylation site"
                                                                                                                                                                                                                                                                                                              phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   site'
           treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                site"
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                                                                                                                                                                                                                                                                                                               site"
                                                                                                                                                                                                                                                                                                                                 site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          site"
                                                                                                                                                                                                                                                                                                                                                                                                                       site
                                                                                                                                                                                                                                                                                                                                                     site"
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RESULT 13
AAB62669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dialysis/pre-dialysis, secondary hyperparathyrodism or osteitis fibrosa cystica, or x-linked hypophosphatemic rickets, hereditary hypophosphatemic rickets with hypercalcuria (HRH), hypomineralised bone lesions, stunted growth in juveniles, oncogenic hypophophatemic osteomalacia, renal phosphate leakage, renal osteodystrophy, osteoporosis, vitamin D resistant rickets, end organ resistance, renal ranconi syndrome, autosomal rickets, Paget's disease, kidney failure, renal tubular acidosis, cystic fibrosis or sprue. The polypeptide may also be used to manufacture combined preparations for simultaneous, separate or sequential use for the treatment of phosphate metabolism disorders. A transformed osteoblast or bone cell line capable of phosphatonin overexpression is useful for the production of
                                                                                                                                                                                                                                                                                                                                                                                                                Metastatic-tumour excreted phosphaturic element; MEPE; phosphate; vitamin-D; skeletal formation; mineralizatio osteopathic; antigout; cytostatic; human.
                                                        Claim 4; Fig
                                                                               skeletal
                                                                                         diagnosing and treating
                                                                                                                                                                 Rowe
                                                                                                                                                                                                             04-NOV-1999;
08-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB62669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 phosphatonin.
                                                                                        New phosphatonin polypeptide a regulator of phosphate metabolism, diagnosing and treating disorders of phosphate, vitamin-D metabol
                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                               31-OCT-2000;
                                                                                                                                                                                                                                                                        10-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB62669
                                                                                                                                                                                       (UNLO ) UNIV COLLEGE
                                                                                                                                                                                                                                                                                              WO200132878-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DXDXSXFXGXXQ
                                                                                                                             2001-343487/36.
DB; AAF83759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNDISPFSGDGQ
                                                                                                                                                                                                                                                                                                                                                                                          sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 6; Conser
                                                                              formation e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphatonin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           430
                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                2000WO-EP10747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
                                                                                                                                                                                                             99US-0434185
99GB-0026424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                                       135pp;
                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers 161..192
                                                                                                                                                                                                                                                                                                                                             /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
50.0%;
                                                                                                                                                                                       LONDON
                                                        English.
                                                                                                                                                                                                                                                                                                                   "the amino acid residues in indicated incorrectly in the in the sequence listing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide (truncated
                                                                               osteoporosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 39;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                               Paget's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..3e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                              mineralization;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEPE).
                                                                               disease,
                                                                                                                                                                                                                                                                                                                                the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                             this region
                                                                                                                                                                                                                                                                                                                                sequence
                                                                              gout
                                                                                                                                                                                                                                                                                                                                                                                                                                        phosphatonin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    430;
                                                                                          metabolism,
                                                                                                                                                                                                                                                                                                                                                                                                                             truncated;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                               provied
                                                                                                                                                                                                                                                                                                                                             are
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                                                                                                    for
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excreted

phosphaturic

relates to a novel human protein, metastatic-tumour phaturic element (MEPE) or phosphatonin (modulator of vitamin-D metabolism). The phosphatonin for treating a

polynucleotides phosphate and

and

specific antibodies are

for treating

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cc mineralization. Phosphatonins are used to treat hyperphosphatemia, renal cc osteodystrophy, secondary hyperparathyroidism, osteitis fibrosa cystica corgout. It is used to prepare a medicament for treating X-linked cc hypophosphatemic rickets, hereditary hypophosphatemic rickets with cc hypophosphatemic rickets, hereditary hypophosphatemic rickets with cc juveniles, oncogenic hypophosphatemic osteomalacia, renal phosphate cc leakage, renal osteodystrophy, osteoporosis, vitamin-D resistant rickets, cc disease, kidney failure, renal fanconi syndrome, autosomal rickets, Paget's cc disease, kidney failure, renal tubular acidosis, cystic fibrosis or cs srue. Phosphatonin polynucleotides are useful as molecular weight cc markers on Southern gels, as diagnostic probes for detecting the presence of a specific mRNA. Phosphatonin polypeptides are also useful for cc identifying agonists and antagonists, compounds which bind to phosphatonin and drug candidates for therapy of phosphate metabolism cc phosphatonin (MEPE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
AAB82922
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Best Local S
Matches 6
                                                                                                                                                                                                   WPI;
 atherosclerotic plaques.
were identified (see also
              polypeptide, i.e. lacking an N-terminal signal sequence. Osteoregulin is a novel protein which plays a role in regulating bone homeostasis, adiposity, and the calcification of atherosclerotic plaques. 2 Splice variants of human osteoregulin
                                                                      The
                                                                                                  Claim
                                                                                                                            measuring
                                                                                                                                      Novel osteoregulin polypeptide useful for regulating bone homeostasis, adiposity and calcification of atherosclerotic plaques comprises
                                                                                                                                                                                                                             Brown
                                                                                                                                                                                                                                                                                  29-FEB-2000; 2000US-185617P
22-SEP-2000; 2000US-234500P
                                                                                                                                                                                                                                                                                                                                                      05-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                 EP1130098-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                    atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Osteoregulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human osteoregulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB82922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB82922 standard; Protein; 509
                                                                                                                                                                                                                                                       (PFIZ
                                                                                                                                                                                                                                                                                                                          27-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \vdash
                                                                     present sequence is that of human osteoregulin mature
                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
                                                                                                                                                                                                 2001-604111/69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNDISPFSGDGQ 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DXDXSXFXGXXQ 12
                                                                                                  ۲.
                                                                                                                                                                                                                                                       ) PFIZER PROD
                                                                                                                                                                                                                           TA,
                                                                                                                                                                                    AAH26810.
                                                                                                  Page
                                                                                                                             the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                          2001EP-0301768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                  54-55.;
                                                                                                                            activity of osteoregulin
                                                                                                                                                                                                                           Wet JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  osteoporosis; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (mature
                                                                                                                                                                                                                                                        NC
                                                                                               90pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               bone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%
    also
                                                                                                                                                                                                                           Gowen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  homeostasis; adipose; calcification;
sis; osteopathic; antiarteriosclerotic;
                                                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6,
                                                                                                                                                                                                                           , 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 39;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                           Hames
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
 invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 430;
provides novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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RESULT 15
AAB82920
ID AAB82920
ID AAB82920
AC AAB8
XX AB8
XX AB8
XX OSte
KW OSte
KW Ather
XX OSTE
FT Pept
FT Prot
FT P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           osteoregulin proteins, nucleic acids which encode them, vectors, antibodies, host cells which express heterologous osteoregulins, and animal cells and mammals with a targeted disruption of an osteoregulin gene. The invention also provides screening assays to identify modulators of osteoregulin activity as well as methods of treating mammals for diseases or disorders associated with osteoregulin activity. The modulators of activity may be useful in the manufacture of a medicament for, as well as for treating, a mammal in need of regulation of bone mass and/or density, adiposity, vascular flexibility, and/or atherosclerotic plaque calcification (claimed), for treating and preventing osteoporosis, and for stimulating bone repair and regeneration.
            The present sequence is that of human osteoregulin, a nover process, which plays a role in regulating bone homeostasis, adiposity, and the calcification of atherosclerotic plaques. The sequence is the calcification of atherosclerotic plaques. The sequence is
                                                                                                                                                                                                Novel osteoregulin polypeptide useful for regulating be adiposity and calcification of atherosclerotic plaques measuring the activity of osteoregulin -
                                                                                                                                                    Claim 1;
                                                                                                                                                                                                                                                                                                    N-PSDB; AAH26808
                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                            Brown TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                             (PFIZ ) PFIZER PROD INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP1130098-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atherosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Osteoregulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human osteoregulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB82920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB82920 standard; Protein; 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       233
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                                                                                                                                                                                                                                                                                                                           2001-604111/69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNDISPFSGDGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DXDXSXFXGXXQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 6; Conser
                                                                                                                                                  Page 45-47;
                                                                                                                                                                                                                                                                                                                                                                            De Wet JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-185617P
2000US-234500P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2001EP-0301768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label=
38..525
/label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          osteoporosis; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                               90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bone; homeostasis;
                                                                                                                                                                                                                                                                                                                                                                            Gowen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6;
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US-09-134-001C-3162
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US-09-332-934-14
US-09-332-934-14
US-09-316-580-12
US-09-614-022-30
US-09-614-022-31
US-09-614-022-31
US-09-614-022-31
US-07-754-918A-6
US-08-461-503-2
US-08-461-503-2
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US-09-106-568E-8
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| 45                | 44                | 43                | 42                | 41                | 40                | 39                | 38                | 37                | 36                | 35                | 34                | 33                | 32                | 31                | 30                | 29                | 28                |
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| 263               | 263               | 263               | 263               | 263               | 263               | 248               | 240               | 177               | 70                | 31                | 20                | 1938              | 833               | 518               | 518               | 518               | 518               |
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| US-08-174-739A-6  | US-08-433-288-6   | US-08-434-418-6   | US-08-413-974-6   | US-08-175-096-4   | US-07-971-096-4   | US-09-032-523-1   | US-09-355-166-19  | US-08-446-920-11  | US-08-847-065-16  | US-08-926-842B-58 | US-08-440-861-35  | US-09-514-302-2   | US-09-514-302-3   | US-09-531-914-9   | US-09-531-914-5   | US-09-531-914-4   | US-09-531-914-3   |
| Sequence 6, Appli | Sequence 6, Appli | Sequence 6, Appli | Sequence 6, Appli | Sequence 4, Appli | Sequence 4, Appli | Sequence 1, Appli | Sequence 19, Appl | Sequence 11, Appl | Sequence 16, Appl | Sequence 58, Appl | Sequence 35, Appl | Sequence 2, Appli | Sequence 3, Appli | Sequence 9, Appli | Sequence 5, Appli | Sequence 4, Appli | Sequence 3, Appli |

### ALIGNMENTS

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Sequence 17, Application US/09242435

Patent No. 6461863

Patent No. 6461863

Patent INFORMATION:

APPLICANT: JARVIS, DONALD L.

TITLE OF INVENTION: MACHIOVIRG INSECT CELL GLYCOSYLATION PATHWAYS WITH

TITLE OF INVENTION: BACULOVIRUS EXPRESSION VECTORS

FILE REFERENCE: UMY0:002US

CURRENT APPLICATION NUMBER: US/09/242,435

CURRENT EILING DATE: 1999-02-16

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 17

LENGTH: 14

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                   APPLICANT: Bhattacharjee, J.
APPLICANT: Suvarna, Kalavati
APPLICANT: Bhattacherjee, Vasker
TITLE OF INVENTION: METHODS AND REAGENTS FOR DETECTING FUN
TITLE OF INVENTION: A BIOLOGICAL SAMPLE
FILE REFERENCE: 96,247-A
CURRENT APPLICATION NUMBER: US/09/106,568E
CURRENT FILING DATE: 1998-06-29
PRIOR APPLICATION NUMBER: 08/650,809
PRIOR APPLICATION NUMBER: 08/650,809
PRIOR FILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Microsoft Word 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of ; OTHER INFORMATION: Peptide US-09-242-435-17
                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/09106568E Patent No. 6455248
LENGTH: 1391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; I
Pred. No. 2
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CURRENT APPLICATION NUMBER: US/09/124,541A
CURRENT FILLING DATE: 1998-07-29
EARLIER APPLICATION NUMBER: 60/054,268
EARLIER FILLING DATE: 1997-07-30
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 534
TYPE: PRT
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Best Local Similarity
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-077-955-29
                                                                                                                                         US-09-124-541-1
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; ORGANISM: Candida albicans
US-09-106-568E-8
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29
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Best Local Similarity 41.7%;
Matches 5; Conservative
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TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
FILE REFERENCE: REG195-B-CCT-US
CURRENT APPLICATION NUMBER: US/09/077,955A
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: PCT/US96/20696
EARLIER FILING DATE: 1996-12-13
EARLIER APPLICATION NUMBER: 08/644,271
EARLIER APPLICATION NUMBER: 08/644,271
EARLIER FILING DATE: 1996-05-10
EARLIER FILING DATE: 1995-12-15
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                                                                                                                                                                                                                                                                                                                               APPLICANT: MOTTIS Ph.D., ROY O. TITLE OF INVENTION: A CYTOKININ OXIDASE FILE REFERENCE: UMO1490
                                                                                                                                                       ORGANISM: Zea mays
409
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                                                                    Conservative
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Pred. No. 1
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Best Local Similarity
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US-09-130-663-30
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US-09-134-001C-3162
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                                                                   Sequence 30, Applicate Patent No. 6020163 GENERAL INFORMATION:
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APPLICANT: TOH, HIPOPUKI
TITLE OF INVENTION: STRUCTURAL ALIGNMENT METHOD MAKING
TITLE OF INVENTION: DYNAMIC PROGRAMMING ALGORITHM
FILE REFERENCE: 9200-0001-2
CURRENT APPLICATION NUMBER: US/08/992,176
CURRENT FILING DATE: 1997-12-17
EARLIER APPLICATION NUMBER: JP 8-340727
EARLIER FILING DATE: 1996-12-20
NUMBER OF SEQ ID NOS: 10
COUNTRY OF THE NOTE OF THE N
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LENGTH: 159
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LENGTH: 633
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Best Local
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APPLICANT: Conklin, Darrell C. TITLE OF INVENTION: LIPOCALIN HOMOLOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:beta-protein
OTHER INFORMATION: (lepb)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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                                                                                                                                              Application US/09130663A
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Pred. No.
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Pred. No. 1.1e+02;
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3.7e+02;
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APPLICANT: Murry, Lynn, E.
APPLICANT: Tang, Tom, Y.
APPLICANT: Tang, Tom, Y.
APPLICANT: Baughn, Mariah, R.
APPLICANT: Bughn, Mariah, R.
TITLE OF INVENTION: LIPOCALIN FAMILY PROTEIN
FILE REFERENCE: PC-005 US
CURRENT APPLICATION UNMBER: US/09/332,934
CURRENT FILING DATE: 1999-06-14
CURRENT FILING DATE: 1999-06-14
CURRENT FILING DATE: 1999-06-14
SOFTWARE: PERL Program
SEQ ID NO 14
                                                                                                                                                                                                                                                       US-09-432-335-30
; Sequence 30, Application US/09432335
; Patent No. 6143720
; GENERAL INFORMATION:
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; LENGTH: 188
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-130-663-30
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                                                            APPLICANT: CONKLIN, Darrell C.
TITLE OF INVENTION: LIPOCALIN HOMOLOG
FILE REFERENCE: 97-24
CURRENT APPLICATION NUMBER: US/09/432,335
CURRENT FILING DATE: 1999-11-02
EARLIER APPLICATION NUMBER: 09/130,663
EARLIER FILING DATE: 1998-08-06
EARLIER APPLICATION NUMBER: 60/054,867
EARLIER FILING DATE: 1997-08-06
EARLIER FILING DATE: 1997-08-06
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 30
LENGTH: 188
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Patent No. 6114123
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OTHER INFORMATION: gll3824
PUBLICATION INFORMATION:
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EARLIER FILING DATE: 1997-08-06
NUMBER OF SEQ ID NOS: 30
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ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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27 DFDISKFLGFW 37
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US-09-614-022-30
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Best Local Similarity
Watches 5; Conserva
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GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 30, Application US/09614022 Patent No. 6365716
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CURRENT FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 09/130,663
PRIOR FILING DATE: 1998-08-06
PRIOR APPLICATION NUMBER: 60/054,867
PRIOR FILING DATE: 1997-08-06
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COMPUTER READABLE FORM:
MEDIUM TYPE: 5 1/4" 360Kb IBM compatible diskette
COMPUTER: IBM PS/2 Model 80
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: Microsoft Word 5.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/754,918A
FILING DATE: 19910905
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENGTH:
                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Stanger,
STREET: Parkway 109
                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                         COUNTRY: UZIP: 07701
                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                      STREET: Road, P. O. CITY: Red Bank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 DEDISKELGEW 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 45.9 5; Conservative
                                                                                                                                                                                                        New Jersey
                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                        RODIIQUEZ,R.S. et al
VENTION: NUCLEOTIDE SEQUENCE CODING FOR AN
VENTION: OUTER MEMBRANE PROTEIN FROM NEISSERIA MENINGITIDIS AND USE
VENTION: OF SAID PROTEIN IN VACCINE PREPARATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87.2%;
45.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.2%;
45.5%;
                                                                                                                                                                                                                                      Michaelson, Spivak and Wallace, Esq
Office Center, 328 Newman Springs
Box 8489
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Pred. No. 1.3e+02;
6; Mismatches 0;
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Pred. No. 1.
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1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 188;
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US-08-316-650-12
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Best Local Similarity
Matches 5; Conserv
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 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (908)530-6584
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1442 amino aci
                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (512) 418-3000 TELEFAX: (713) 789-2679
                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/199,780 FILING DATE: 30-SEP-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/316,650
FILING DATE: 30-SEP-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: Sequence which includes variable regions MOLECULE TYPE: P1.15 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: Ce
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)530-6671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: METHODS AND COMPOSITIONS TITLE OF INVENTION: FOR STIMULATING BONE CELLS
                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                           TELEFAX: (, 79-0924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                           STRANDEDNESS:
                                                                                                                                                                                                                     NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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5942496
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AMINO ACID
                                                                                            amino acid
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                                                                                                         1442 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (908)530-6584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lin, Wushan
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                                                                           single
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45.5%;
   84.6%;
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                                                                                                                                           12:
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 Score 33;
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Pred. No. 2
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2.5e+02;
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2
 Length 1442;
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Query Match
Best Local Similarity
Watches 5; Conserve
                                                                          RESULT 14
US-07-852-260-2
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PCT-US95-02251-12
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                                            Sequence 2, Application US/07852260 Patent No. 5525715
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GENERAL INFORMATION:
APPLICANT: Racania
APPLICANT: Tatem,
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Matches 5; Conserva
                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                        1173 IDMSAFAGLGQ 1183
                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: UM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEPAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/316,650
FILING DATE: 30-SEP-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                             TYPE: amino acids
STRANDEDNESS: single
TOPOLOGY
                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (/13)
                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/199,780 FILING DATE: 18-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: CONCU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Houston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Texas
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Racaniello, Vincent Tatem, Joanne M.
                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                           linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMBER: PCT/US95/02251
CONCURRENTLY HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                 84.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METHODS AND COMPOSITIONS FOR STIMULATING BONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             32,165
                                                                                                                                                                                                                                                                                                                                                                                                                                               UMIC009P--
                                                                                                                                                                                                  6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6,
                                                                                                                                                                                                                 Score 33; I
Pred. No. 2
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6; Mismatches 0;
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                                                                                                                                                                                                                 DB 5;
2.3e+03;
                                                                                                                                                                                                                               Length 1442;
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US-08-461-503-2
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NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 36607-B-PCT-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 977-9550

TELEFAX: (212) 664-0525

TELEFAX: (212) 664-0525

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 2206 amino acids

TYPE: AMINO ACID

TOPOLOGY: 11 near
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Floppy disk
COMPUTER: IBM PC COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/852,260
FILING DATE: 19920619
CLASSIFICATION: 435
ATTORNEY/AGFNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 84.6%;
Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Applicati Patent No. 5834302 GENERAL INFORMATION:
               COMPUTER READABLE FORM:
MEDIUM TYPE: FORDY disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC - DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/461,503
FILING DATE: 5-UN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1283 PDPSHFDGYKQ 1293
                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Racaniello, Vincent
APPLICANT: Tatem, Joanne M.
APPLICANT: Weeks-Levy, Carolyn L.
TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES
TITLE OF INVENTION: FROM CDNA
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM
TITLE OF INVENTION: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                         STREET: 1185 AVE
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
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CITY: New York
STATE: New Yor)
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Y: U.S.A.
                                                                                                                                                                                                                                                                                         1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cooper & Dunham
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Pred. No. 3.8e+03;
6; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.
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; MOLECULE TYPE: protein US-08-461-503-2
Search completed: March 18, 2003, 08:32:22 Job time: 12.5 secs
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                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 3660
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2206 amino acids
TYPE: amino acid
                                                                                                                                      Query Match 84.6%;
Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                     1283 PDPSHFDGYKQ 1293
                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: White, John P. REGISTRATION NUMBER: 28,678
                                                                                                      2 XDXSXFXGXXQ 12
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Pred. No. 3.8e+03;
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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
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                                                                                                                                                                                                                                                                                               Score
                                                                                                       48
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110:
      Match
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNDISPFSGDGQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
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US-09-812-485A-48
US-09-812-485A-30
US-09-811-485A-36
US-09-812-485A-26
US-09-812-485A-26
US-09-812-485A-26
US-09-812-485A-24
US-10-192-584-7
US-10-192-584-7
US-10-192-584-7
US-10-192-584-7
US-10-108-605-125
US-09-815-447-70
US-09-815-447-70
US-10-108-605-125
US-10-108-605-125
                                                                                                                                                                                                     US-09-812-485A-42
US-09-812-485A-47
US-09-812-485A-49
US-09-812-485A-23
US-09-812-485A-1
                                                                                                                                                                                                                                                                                                                                        SUMMARIES
Sequence 42, Appl
Sequence 47, Appl
Sequence 23, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 30, Appl
Sequence 30, Appl
Sequence 6, Appl
Sequence 26, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 77, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 70, Appl
Sequence 71, Appl
Sequence 72, Appl
Sequence 73, Appl
Sequence 74, Appl
Sequence 75, Appl
Sequence 76, Appl
Sequence 77, Appl
Sequence 77, Appl
Sequence 78, Appl
Sequence 79, Appl
Sequence 79, Appl
                                                                                                                                                                                                                                                                                            Description
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| 45                | 44                | 43                | 42                | 41                | 40                | 39                | 38              | 37                | 36                  | 35                 | 34                | 33                | 32                | 31                 | 30                  | 29                | 28                | 27                | 26               | 25                | 24                | 23                | 22                  | 21                | 20                |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----------------|-------------------|---------------------|--------------------|-------------------|-------------------|-------------------|--------------------|---------------------|-------------------|-------------------|-------------------|------------------|-------------------|-------------------|-------------------|---------------------|-------------------|-------------------|
| 34                | 34                | 34                | 34                | 34                | 34                | ω<br>5            | 3<br>5          | 35                | <u>ω</u>            | ა<br>5             | 35                | 35                | 35                | 35                 | 35                  | 36                | 36                | 36                | 36               | 36                | 36                | 36                | 36                  | 36                | 37                |
|                   |                   | •                 |                   |                   | •                 |                   |                 |                   |                     |                    |                   |                   | 53.0              |                    |                     |                   | •                 | •                 | •                |                   |                   |                   | •                   |                   | 56.1              |
| 290               | 182               | 147               | 147               | 58                | 17                | 607               | 607             | 532               | 450                 | 326                | 240               | 205               | 188               | 188                | 114                 | 912               | 912               | 906               | 906              | 906               | 877               | 623               | 437                 | 413               | 1198              |
| 10                | 10                | 10                | 10                | 10                | 10                | 10                | 10              | 10                | 10                  | 9                  | 10                | 10                | 10                | 10                 | 10                  | 10                | 10                | 10                | 10               | 10                | 10                | 10                |                     | 10                | 9                 |
| US-09-925-297-817 | US-09-784-810A-29 | US-09-844-736-6   | US-09-797-481-4   |                   | US-09-861-294-33  | US-09-801-196-29  | US-09-734-002-2 | US-09-891-160-2   | US-09-815-242-13497 | US-09-738-626-4959 | US-09-950-368-19  | US-09-841-132-564 | J.                | US-09-815-242-4981 | US-09-864-761-36859 | US-09-746-491-49  |                   | -746-491-         | US-09-746-491-46 | -983              | US-09-746-491-47  |                   | US-09-815-242-11837 | US-09-746-491-43  | US-09-975-719-405 |
| Sequence 817, App | Sequence 29, Appl | Sequence 6, Appli | Sequence 4, Appli | Sequence 40191, A | Sequence 33, Appl | Sequence 29, Appl | •               | Sequence 2, Appli | Sequence 13497, A   |                    | Sequence 19, Appl | Sequence 564, App | Sequence 10949, A | Sequence 4981, Ap  | Sequence 36859, A   | Sequence 49, Appl | Sequence 2, Appli | Sequence 48, Appl | 46,              | Sequence 46, Appl | Sequence 47, Appl | Sequence 13499, A | Sequence 11837, A   | Sequence 43, Appl | Sequence 405, App |

# ALIGNMENTS

RESULT 1 US-09-812-485A-42

```
GENERAL INFORMATION: OSCIPLIANT:

APPLICANT: Blacher, Russel

APPLICANT: Blacher, Russel

APPLICANT: Voneda, Toshiyuki

TITLE OF INVENTION: Integrin Binding Motif Containing

TITLE OF INVENTION: Integrin Binding Motif Containing

FILE REFERENCE: BEAR-006CIP

CURRENT APPLICATION NUMBER: US/09/812,485A

CURRENT FILING DATE: 2001-03-19

PRIOR APPLICATION NUMBER: US/09/812,485A

PRIOR APPLICATION NUMBER: US/09/812,485A

PRIOR FILING DATE: 2000-08-16

NUMBER: OF SEQ ID NOS: 50

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                       RESULT 2
US-09-812-485A-47
                                                                                                                                                                                                                                         Q
                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: calcium binding motif US-09-812-485A-42
                                                                                                                                                                                                       밁
Sequence 47, Application US/09812485A
Publication No. US20020197267A1
GENERAL INFORMATION:
APPLICANT: Kunagai, Yoshinari
APPLICANT: Blacher, Russel
APPLICANT: Yoneda, Toshiyuki
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Watches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 42, Application Publication No. US2002019
                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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1 DNDISPFSGDGQ 12
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US20020197267A1
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                                                                                                                                                                                                                                                                                                   Score 66;
Pred. No.
                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                     Length 12;
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0;

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RESULT 4
US-09-812-485A-23
Sequence 23, Application US/09812485A
Publication No. US20020197267A1
GENERAL INFORMATION:
APPLICANT: Kunagai, Yoshinari
APPLICANT: Blacher, Russel
APPLICANT: Yoneda, Toshiyiki
APPLICANT: Yoneda, Toshiyiki
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                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Kumagai, Yoshinari
APPLICANT: Kumagai, Yoshinari
APPLICANT: Blacher, Russel
APPLICANT: Yoneda, Toshiyuki
TITLE OF INVENTION: Integrin Binding Motif Containing
TITLE OF INVENTION: Peptides and Methods of Treating
FILE REFERENCE: BEAR-006CIP
CURRENT APPLICATION NUMBER: US/09/812,485A
CURRENT FILING DATE: 2001-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 09/641,034
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 49, Application US/09812485A publication No. US20020197267A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Integrin Binding Motif Containing TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases FILE REFERENCE: BEAR-006CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 09/641,034
PRIOR FILING DATE: 2000-08-16
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TITLE OF INVENTION: Integrin Binding Motif Containing
                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 23
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: D-00006 peptide NAME/KEY: AMIDATION LOCATION: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: AMIDATION LOCATION: 15
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                                                                                                                                                                                                                                                                                                      Score 66;
Pred. No.
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Pred. No.
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APPLICANT: Levine, MILING BEUT, SUZANNE
APPLICANT: Jan de Beur, SUZANNE
TITLE OF INVENTION: ONCOGENIC OSTEOMALACIA-RELATED
FILE REFERENCE: 5014US
CURRENT APPLICATION NUMBER: US/09/814,550
CURRENT FILING DATE: 2001-03-22
                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09812485A Publication No. US20020197267A1 GENERAL INFORMATION:
                                                                                                                                                                                                                 Sequence 2, Application US/09814550 Patent No. US20020102641A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 23
LENGTH: 40
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                                                                                                                                         APPLICANT: Manavalan, Part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/812,485A CURRENT FILING DATE: 2001-03-19 PRIOR APPLICATION NUMBER: 09/641,034 PRIOR FILING DATE: 2000-08-16 NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kumagai, Yoshinari
APPLICANT: Blacher, Russel
APPLICANT: Yoneda, Toshiyuki
TITLE OF INVENTION: Integrin Binding Motif Containing
TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases
FILE REFERENCE: BEAR-006CIP
                                                                                                                                                                            APPLICANT: Schiavi, Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/812,485A CURRENT FILING DATE: 2001-03-19 PRIOR APPLICATION NUMBER: 09/641,034 PRIOR FILING DATE: 2000-08-16 NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases FILE REFERENCE: BEAR-006CIP
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TYPE: PRT
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12; Conserv
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Pred. No.
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Pred. No. 0.00026;
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; SEQ ID NO 2
; LENGTH: 525
; TYPE: PRT
; ORCANISM: Homo sapiens
US-09-814-550-2
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Best Local Similarity
Whiches 11; Conserve
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Sequence 30, Application US/09812485A
Publication No. US20020197267A1
GENERAL INFORMATION:
APPLICANT: Kumagai, Yoshinari
APPLICANT: Vaneda, Toshiyuki
TITLE OF INVENTION: Integrin Binding Motif Containing
TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases
FILE REFERENCE: BEAR-006CIP
CURRENT APPLICATION NUMBER: US/09/812,485A
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 09/641,034
PRIOR APPLICATION NUMBER: 09/641,034
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 50
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APPLICANT: Yoneda, Toshiyuki
TITLE OF INVENTION: Integrin Binding Motif Containing
TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases
FILE REFERENCE: BEAR-006CIP
CURRENT APPLICATION NUMBER: US/09/812,485A
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 09/641,034
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 50
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APPLICANT: Blacher, Russel
APPLICANT: Yoneda, Toshiyuki
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PRIOR APPLICATION NUMBER: US 60/241,598
PRIOR FILING DATE: 2000-10-19
NUMBER OF SEQ ID NOS: 8
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ORGANISM: Artificial Sequence
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Pred. No.
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                                                                                                GENERAL INFORMATION:

APPLICANT: Kumagai, Yoshinari

APPLICANT: Kumagai, Yoshinari

APPLICANT: Blacher, Russel

APPLICANT: Yoneda, Toshiyuki

TITLE OF INVENTION: Integrin Binding Motif Containing
TITLE OF INVENTION: Peptides and Methods of Treating
FILE REPERENCE: BEAR-006CIP

FULE REPERENCE: BEAR-006CIP

CURRENT APPLICATION NUMBER: US/09/812,485A

CURRENT FILING DATE: 2001-03-19

CURRENT FILING DATE: 2001-03-19
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SEQ ID NO 26
LENGTH: 30
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Best Local Similarity
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                               PRIOR APPLICATION NUMBER: 09/641,034
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Versio
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PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/241,598
PRIOR ETLING DATE: 2000-10-19
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin version 3.0
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TITLE OF INVENTION: ONCOGENIC OSTEOMALACIA-RELATED GENE
FILE REFERENCE: 5014US
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TYPE: PRT
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TYPE: PRT
ORGANISM: Artificial
FEATURE:
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Pred. No.
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                                                                                                             NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
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Best Local Similarity
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                                                                                                                                                                TITLE OF INVENTION: Integrin Binding Motif Containing
TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases
FILE REFERENCE: BEAR-006CIP
CURRENT APPLICATION NUMBER: US/09/812,485A
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 09/641,034
PRIOR FILING DATE: 2000-08-16
                                                                                                                                                                                                                                                                                                     APPLICANT: Blacher, Russel APPLICANT: Yoneda, Toshiyuki
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APPLICANT: Yoneda, Toshiyuki
TITLE OF INVENTION: Integrin Binding Motif Containing
TITLE OF INVENTION: Peptides and Methods of Treating
FILE REFERENCE: BEAR-006CIP
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kumagai, Yoshinari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 50 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·09-812-485A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kumagai, Yoshinari
               OTHER INFORMATION: peptidic compound
                                                     ORGANISM: Artificial Sequence
                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 NDISPF---SGDGQ 12
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                                                                                             40
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78.6%;
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100.0%;
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Pred. No.
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0.056;
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RESULT 14
US-10-192-584-6
· Sequence 6, Application US/10192584
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US-10-192-584-7
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Best Local
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Best Local
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SOFTWARE: Patent In Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION SHOPE
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: JP 27,148/1996
FILING DATE: 19-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: KORNIAU, Anne M.
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/10/192,584
FILING DATE: 11-Jul-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/077,098
FILING DATE: 19-May-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOKIYOSHI, Sachio
TITLE OF INVENTION: NOVEL POLYPEPTIDE FROM HAEMOPHILUS
PARAGALLINARUM AND PROCESS FOR PREPARING THE SAME
                                                                                                                                                                                                                                               MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: 9
                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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ADDRESSEE: BROWDY AND NEIMARK
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                                                                                                          DGDISPTSGD 1608
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                                                                                                                                                                   Similarity 80.08; Conservative
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                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/JP97/03222
FILING DATE: 12-SEP-1997
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HAMADA, Fukusaburo
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80.0%;
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Pred. No.
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TOPOLOGY: Inear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-192-584-6
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US-09-812-485A-46
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Sequence 46, Application US/09812485A
Publication No. US20020197267A1

GENERAL INFORMATION:

APPLICANT: Kunagai, Yoshinari
APPLICANT: Yoneda, Toshiyuki
TITLE OF INVENTION: Integrin Binding Motif Containing
TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases
FILE REFERENCE: BEAR-006CIP
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: US/09/812,485A
CURRENT FILING DATE: 2000-08-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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1591 DGDISPTSGD 1600
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Ver
CURRENT APPLICATION NUMBER: US/10/192/584
FILING DATE: 11-Jul-2002
PRIOR APPLICATION UNMEER: US/09/077,098
FILING DATE: 19-May-1998
APPLICATION NUMBER: PCT/JP97/03222
FILING DATE: 12-SEP-1997
APPLICATION NUMBER: JP 27,148/1996
FILING DATE: 19-SEP-1996
APPLICATION NUMBER: JP 27,148/1996
FILING DATE: 19-SEP-1996
APPLICATION DATE: 19-SEP-1996
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NAME: KORNBAU, Anne M.
REGISTRATION NUMBER: 25,618
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ADDRESSEE: BROWDY AND NEIMARK
STREET: 624 Ninth Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
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HAMADA, Fukusaburo
HAMADA, Fukusaburo
TOKIYOSHI, Sachio
TITLE OF INVENTION: NOVEL POLYPEPTIDE FROM HAEMOPHILUS
PARAGALLINARUM AND PROCESS FOR PREPARING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: TOKUNAGA, Eiji
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Similarity 80.0%;
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41; DB 9
Pred. No. 93;
0; Mismatches
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Search completed: March 18, 2003, 08:32:50 Job time: 12 secs
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                                                                                                                                                               US-09-812-485A-46
                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46
LENGTH: 15
TYPE: PRT
                                                                                                    Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                            OTHER INFORMATION: D-00003 peptide NAME/KEY: AMIDATION LOCATION: 15
                                                                                                                                                                                                                  ORGANISM: Artificial FEATURE:
                                                       9 DNDISPF 15
                                                                                1 DNDISPF 7
                                                                                                          Conservative
                                                                                                                                                                                                                               Sequence
                                                                                                       59.1%; Score 39;
100.0%; Pred. No.
Live 0; Mismatc
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1.3;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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seq length:
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          Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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             US-09-812-485A-42
US-09-812-485A-43
US-09-812-485A-47
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US-09-812-485A-23
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US-09-812-485A-23
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1 US-09-819-666661
1 US-09-829-549A-48
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                                                Sequence 42, Appl
Sequence 47, Appl
Sequence 49, Appl
Sequence 19, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 8, Appl
Sequence 87, Appl
Sequence 87, Appl
Sequence 87, Appl
Sequence 48, Appl
Sequence 5, Appl
Sequence 191, Appl
Sequence 191, Appl
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     Sequence 191, App
Sequence 16, Appl
Sequence 5227, Ap
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| 45                | 44                | 43                 | 42                 | 41                | 40                 | 39               | 38                | 37                 | 36                 | 3<br>5           | 34                  | 33                 | 32                 | 31                 | 30                | 29                  | 28                  | 27                | 26                | 25                | 24                | 23                | 22                  | 21                  | 20                  |  |
|-------------------|-------------------|--------------------|--------------------|-------------------|--------------------|------------------|-------------------|--------------------|--------------------|------------------|---------------------|--------------------|--------------------|--------------------|-------------------|---------------------|---------------------|-------------------|-------------------|-------------------|-------------------|-------------------|---------------------|---------------------|---------------------|--|
| 32                | 32                | 32                 | 32                 | 32                | 32                 | 32               | 32                | 32                 | 32                 | 32               | 33                  | 33                 | 33                 | 33                 | 33                | 33                  | ω<br>ω              | ω<br>ω            | <b>ω</b>          | ω<br>S            | 34                | 34                | 34                  | 34                  | 34                  |  |
|                   | 82.1              |                    |                    |                   |                    |                  |                   |                    |                    |                  |                     |                    |                    |                    |                   |                     |                     |                   |                   |                   |                   |                   |                     |                     |                     |  |
| 833               | 727               | 655                | 518                | 497               | 478                | 315              | 315               | 311                | 233                | 142              | 722                 | 500                | 500                | 484                | 270               | 66                  | 59                  | <b>ω</b>          | 19                | 15                | 1325              | 1138              | 436                 | 432                 | 432                 |  |
| 9                 | 10                | 9                  | 10                 | 10                | 9                  | 10               | 9                 | 9                  | 10                 | 10               | 10                  | 9                  | 9                  | 9                  | 10                | 10                  | 10                  | 9                 | 10                | 9                 | 10                | 10                | 10                  | 10                  | 10                  |  |
| US-10-014-436-3   | US-09-822-246-2   | US-09-738-626-5440 | US-09-771-161A-231 | US-09-862-027-8   | US-09-866-050A-512 | US-09-847-809A-3 | US-09-984-245-200 | US-09-738-626-3862 | US-09-925-300-1529 | US-09-862-027-31 | US-09-815-242-10796 | US-09-738-626-6393 | US-09-738-626-4296 | US-09-738-626-6755 | US-09-911-826A-8  | US-09-864-761-46305 | US-09-864-761-39774 | US-09-812-485A-30 | US-09-814-550-6   | US-09-812-485A-48 | US-09-741-669-304 | US-09-767-215-5   | US-09-815-242-11154 | US-09-815-242-13866 | US-09-815-242-10274 |  |
| Sequence 3, Appli | Sequence 2, Appli | Sequence 5440, Ap  | 231                | Sequence 8, Appli | 2                  |                  | Sequence 200, App | w                  | Sequence 1529, Ap  |                  | e 10796             | Sequence 6393, Ap  | 4296,              | Sequence 6755, Ap  | Sequence 8, Appli | Sequence 46305, A   | Sequence 39774, A   | Sequence 30, Appl | Sequence 6, Appli | Sequence 48, Appl | 30,               | Sequence 5, Appli | Sequence 11154, A   | Sequence 13866, A   | Sequence 10274, A   |  |

## ALIGNMENTS

RESULT 1 US-09-812-485A-42

Sequence 42, Application US/09812485A Publication No. US20020197267A1

GENERAL INFORMATION:

APPLICANT: Kumagai, Yoshinari
APPLICANT: Blacher, Russel
APPLICANT: Yoneda, Toshiyuki
TITLE OF INVENTION: Integrin Binding Motif Containing
TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases
FILE REFERENCE: BEAR-006CIP

CURRENT APPLICATION NUMBER: US/09/812,485A
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 09/641,034
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEO ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
SEO ID NO 42
LENGTH: 12

TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:

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RESULT 2
US-09-812-485A-43
                                                                                                                                                                                                                                    ; OTHER INFORMATION: calcium binding motif US-09-812-485A-42
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                                    Sequence 43, Application US/09812485A Publication No. US20020197267A1 GENERAL INFORMATION:
                                                                                                                                                                                             Best
                                                                                                                                                                                  Matches
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APPLICANT: Kumagai, Yoshinari
APPLICANT: Blacher, Russel
APPLICANT: Yoneda, Toshiyuki
                                                                                                                                                                                 Local Similarity
les 6; Conserv
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DNDISPFSGDGQ 12
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RESULT 4
US-09-812-485A-49
Sequence 49, Application US/09812485A
Publication No. US20020197267A1
GENERAL INFORMATION:
APPLICANT: Kumagal, Yoshinari
APPLICANT: Blacher, Russel
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Best Local S
Matches 12
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PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 47, Application US/09812485A Publication No. US20020197267A1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 43
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APPLICANT: Yoneda, Toshiyuki
TITLE OF INVENTION: Integrin Binding Motif Containing
TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases
FILE REFERENCE: BEAR-006CIP
CURRENT APPLICATION NUMBER: US/09/812,485A
CURRENT FILING DATE: 2001-03-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Integrin Binding Motif Containing TITLE OF INVENTION: Peptides and Methods of Treating Skeletal Diseases FILE REFERENCE: BEAR-006CIP CURRENT APPLICATION NUMBER: US/09/812,485A CURRENT FILLING DATE: 2001-03-19 PRIOR APPLICATION NUMBER: 09/641,034 PRIOR APPLICATION NUMBER: 09/641,034 PRIOR EPILING DATE: 2000-08-16
   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kumagai, Yoshinari
                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: D-00004 peptide NAME/KEY: AMIDATION LOCATION: 15
                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: VARIANT LOCATION: 2, 4, 6,
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Blacher, Russel
Yoneda, Toshiyuki
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Sequence 1, Application US/09812485A
Publication No. US20020197267A1
GENERAL INFORMATION:
APPLICANT: Kunagai Yoshinari
APPLICANT: Blacher, Russel
APPLICANT: Yoneda, Toshiyuki
TITLE OF INVENTION: Integrin Binding Motif Containing
TITLE OF INVENTION: Peptides and Methods of Treating
FILE REFERENCE: BEAR-006CIP
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                                                                                                                                                               RESULT 6
US-09-812-485A-1
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Best Local Similarity
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LENGTH: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/641,034
PRIOR FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Fastern 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kumagai, Yoshinari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Yoneda, Toshiyuki
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: peptidic compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: AMIDATION LOCATION: 15
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Pred. No. 1
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CURRENT APPLICATION NUMBER: US/09/812,485A;
CURRENT FILLING DATE: 2001-03-19;
PRIOR APPLICATION NUMBER: 09/641,034
PRIOR FILING DATE: 2000-08-16;
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FASTSEQ for Windows Version 4.0;
SEQ ID NO 1
LENGTH: 97
TYPE: PRT
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APPLICANT: Madden, Stephen
APPLICANT: Manavalan, Parthasara
APPLICANT: Levine, Michael
APPLICANT: Jan de Beur, Suzanne
TITLE OF INVENTION: ONCOGENIC OST
FILE REFERENCE: 5014US
                                                                                                                                          Sequence 1173, Application Patent No. US20020132753A1 GENERAL INFORMATION:
Prior application data removed -
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1173
                                                                                                                                                                                                                                                                                                                                                  Query Match
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Best Local :
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                                                             APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/814,550 CURRENT FILING DATE: 2001-03-22 PRIOR APPLICATION NUMBER: US 60/191,786 PRIOR FILING DATE: 2000-03-24 PRIOR APPLICATION NUMBER: US 60/241,598 PRIOR FILING DATE: 2000-10-19
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SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No.
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Pred. No. 9
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US-09-994-595-8
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US-09-767-215-2
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                                                                                  GENERAL INFORMATION:
                                                                                                Sequence 8, Application US/09994595 Publication No. US20030039981A1
                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version SEQ ID NO 2
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APPLICANT: Bhattacharjee, J. APPLICANT: Suvarna, Kalavati APPLICANT: Suvarna, Kalavati APPLICANT: Bhattacherjee, Vasker TITLE OF INVENTION: METHODS AND REAGENTS FOR DETECTING FUNGAL PATHOGENS TITLE OF INVENTION: A BIOLOGICAL SAMPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/767,215
CURRENT FILING DATE: 2001-01-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF FILE REFERENCE: 07334-142001
                                                                                                                                                                                                                                                                                                                                                 LENGTH: 10
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2001-01-22 PRIOR APPLICATION NUMBER: 60/181,159 PRIOR FILING DATE: 2000-02-09
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NAME/KEY: SITE
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OTHER INFORMATION:
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LOCATION: (216)
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Pred. No. 4.5e+02;
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REFERENCE:

96,247-A

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RESULT 12
US-09-886-055-87
US-09-886-055-87
; Sequence 87, Application US/09886055
; Patent No. US20020132273A1
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Best Local Similarity
Thes 5; Conserve
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PRIOR FILING DATE: 1997-05-20
NUMBER OF SEQ ID NOS: 160
SOFTWARE: Microsoft Word 97
SEQ ID NO 8
LENGTH: 1391
TYPE: PRT
ORGANISM: Candida albicans
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                                                        SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 87
                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                       PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 522
                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/886,055
CURRENT FILING DATE: 2001-06-22
                                                                                                                                                                                     TITLE OF INVENTION: RECEPTOR FINGERPRINTING, SENSORY PERCEPTION, AND TITLE OF INVENTION: BIOSENSORS OF CHEMICAL SENSANTS FILE REFERENCE: 078003-0277150
                                                                                                            PRIOR APPLICATION NUMBER: 60/213,812 PRIOR FILING DATE: 2000-06-22
                                                                                                                                                                                                                                        APPLICANT: STRYER, LUBERT
APPLICANT: ZOZULYA, SERGEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US/09/077,955A
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: PCT/US96/20696
PRIOR FILING DATE: 1996-12-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Valenzuela et al., David M.
TITLE OF INVENTION: NOVEL TYROSINE KINASE RECEPTORS AND LIGANDS
FILE REFERENCE: REG195-B-PCT-US
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CURRENT FILING DATE: 2001-11-30
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CURRENT FILING DATE: 2001-11-27
                       TYPE: PRT
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ORGANISM: Homo sapiens
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41.7%;
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41.7%;
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Pred. No.
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Pred. No. 6.
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1.7e+02;
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Best Local Similarity
Thes 5; Conserve
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; LOCATION: (68)
; OTHER INFORMATION: Variable amino US-09-886-055-87
                                                                                                                           RESULT 14
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PEDICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
                                                     GENERAL INFORMATION:
                                                                   Sequence 6061, Application US/09738626 Publication No. US20020197605A1
                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5214
                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                 APPLICANT: NAKAGAWA, SATOSHI
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                  APPLICANT:
 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-12-22
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PRIOR FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE:
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ANDO, SEIKO
                  MIZOGUCHI,
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Yamamoto, Robert T.
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Zyskind, Judith W.
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Pred. No.
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2.7e+02;
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APPLICANT:

HAYASHI, MIKIRO

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RESULT 15
US-09-829-549A-48
US-09-829-549A-8
; Sequence 48, Application US/09829549A
; Patent No. US20020052484A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6061
; LENGTH: 536
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6061
      В
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APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                       NAME/KEY: SIGNAL
LOCATION: (1)..(85)
COTHER INFORMATION: Mat-alpha secretory sequence
NAME/KEY: DOMAIN
LOCATION: (86)..(600)
OTHER INFORMATION: Cytokinin oxidase 1
NAME/KEY: DOMAIN
LOCATION: (601)...(602)
OTHER INFORMATION: Linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: The Curators of the University of Missouri
TITLE OF INVENTION: PHAGE DISPLAY SELECTION OF ANTI FUNGAL PEPTIDES
FILE REFERENCE: UMO 1521.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.0
SEQ ID NO 48
LENGTH: 611
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Best Local Similarity
Matches 5; Conserv
                                                                             Best Local Similarity 41.7
Matches 5; Conservative
                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/829,549A CURRENT FILING DATE: 2001-04-10 PRIOR APPLICATION NUMBER: US 60/195,785 PRIOR FILING DATE: 2000-04-10
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                                                                                                                                                                      NAME/KEY: DOMAIN
LOCATION: (603)..(611)
OTHER INFORMATION: Random peptide Pc 87
                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
|:|: :|:|::|
475 DFDRGVFKGILQ 486
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315 EWDLSEFVGDIQ 326
                                      1 DXDXSXFXGXXQ 12
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TATEISHI, NAOKO
SENOH, AKIHIRO
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nilarity 41.7%;
Conservative
                                                                                                 89.7%;
41.7%;
                                                                             Score 35; DB 10;
Pred. No. 3.8e+02;
6; Mismatches 1
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                                                                                                               DB 10; Length 611;
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Search completed: March 18, 2003, 08:32:51 Job time : 12 secs

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Result
No.
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Maximum DB seq length: 2000000000
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Perfect score:
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.
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US-09-812-485A-43
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probable secreted hypothetical proteconserved hypothet vacuolar ATP synth atrial gland pepti

RESULT 2 T37881 entochondrial import receptor chain SPAC17H9.16 - fission yeast (Schizosacchar) C;Species: Schizosaccharomyces pombe

| Oy 1 [                           | Query Match<br>Best Local<br>Matches              | Gene:<br>Cross-<br>Map po            |  |                                    | A; Molecule type: DNA A; Residues: 1-233 <rie> A; Cross-references: EMBL: Z729 A; Experimental source: strain</rie> | R; Rieger, M.; Muell<br>submitted to the Pr<br>A; Reference number:<br>A; Accession: S64478 | A; Accession: B36425<br>A; Molecule type: pr<br>A; Residues: 31-39 < | A; Accession<br>A; Molecule<br>A; Residues:      | J. Cell Bio A; Title: Ye A; Reference                                | C;species: saccinatomyces cerevis<br>C;Date: 17-Apr-1991 #sequence_re<br>C;Accession: A36425; B36425; S64<br>R;Silveira, L.A.; Wong, D.H.; Ma                             | RESULT 1 A36425 clathrin li N; Alternate               |            | 444<br>444<br>45   | 39<br>41   | 36<br>37<br>38  | ယ ယ ယ<br>Մ <b>4</b> ယ  | 30<br>31<br>32                     |
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| )XDXSXFX<br> : : : :<br>)DDFSTFE |   | SGD:CLC1;<br>reference<br>rsition: 7 | type:<br>10-2<br>erencental s  | to the ce numb                     | type:<br>: 1-23<br>:erenc   | 1.; Mu<br>to the<br>numb  | type:  | type:  | east central   | Apr-1<br>Apr-1<br>1: A36  | ight c   |            | 344  | ω ω ω<br>4 4 4   | 34<br>4<br>4<br>4                                     | ω ω ω<br>4 4 4   | 34                                 |
| GXXQ<br>F:: <br>GANQ             | n<br>Similarity 50.<br>6; Conservative            | L 2                                  | DNA<br>33 <heb><br/>es: EMBL</heb>   | the Protein S<br>number: S64003    |   | Mueller-Auer, S.; Buthe Protein Sequence number: S64071                                     | 1: B36425<br>type: protein<br>: 31-39 <si2></si2>                    | DNA<br>SIL>                                      | lathrin<br>er: A36   | saccinaromyces cerevisiae Apr-1991 #sequence_revis n: A36425; B36425; S64478 L.A.; Wong, D.H.; Masia  | hain -   |            | 87.2<br>87.2<br>87.2   | 87.2<br>87.2   | 7.  | 77.  | 7.                                 |
| 12<br>108                        | 100.<br>50.0<br>7ative                            | D4<br>SGD:S0003399;                  | ><br>L:Z7295<br>strain   | B.; Delius,<br>n Sequence D<br>003 | (IE><br>EMBL:272952;<br>e: strain S2  | uer, S.<br>n Seque<br>071   | n 20474,   | <b>46</b> 22 22 22 22 22 22 22 22 22 22 22 22 22 | has a 425; MU  | quence<br>6425; S   | yeast (<br>ein G70                                     |            | 326<br>329<br>332  |  |   |  |                                    |
|                                  | **  | 99;                                  | 2; 1<br>S281   | lius                               | œ   | nce   | 2  | 1  | dist   | rev<br>644  | Sacr   |            | 0000   |  |   |  |                                    |
|                                  | Score 39; DB 2;<br>Pred. No. 18;<br>6; Mismatches | MIPS:YGR167w                         | Molecule type: DNA Residues: 10-233 <heb> Cross references: EMBL: 272952; MIPS:YGR167w Experimental source: strain S288C Genetics:</heb> | s, H.<br>Database, May 1996        | D:g1323293;   | rueckner, M.;<br>Database, May  | NID GOOTH, EIDN:CWOODID  |  | , 1990<br>a distinctive light chain t<br>MUID:91009480; PMID:2211819 | <pre>is: baccharomyces cerevisiae 12-Apr-1991 #sequence_revision 12-Apr-1991 #te ion: A36425; B36425; S64478; S64481 ra, L.A.; Wong, D.H.; Masiarz, F.R.; Schekman,</pre> | st (Saccharomyces cerevisiae<br>G7056; protein YGR167w | ALIGNMENTS | C83259<br>T10683<br>A81675                                     | AB2768<br>D97548<br>B69073                             | E97427<br>S22401<br>S22400                            | AE2645<br>SQRTAD<br>CUWOI                                      | B45932<br>GOGABA<br>S21380         |
|                                  | Length<br>0; Inde:                                |                                      |  | 96                                 | PIDN:CAA97192.1;  | Schaefer, M.<br>1996  | . 1  |  | hat  | <pre>#text_change man, R.</pre>   | siae)  |            | ס סיב מ  |  | P• F• F•  | P- Ø F+  | rh Qu Qu                           |
|                                  | 33;   |                                      |  |                                    | .1; PID:e243718;  |   | 7 E C C C C C C C C C C C C C C C C C C                              | 200  | is important   | nge 29-Oct-1999   |  |            | probable phosphoes<br>hypothetical prote<br>conserved hypothet | lipoate biosyntl<br>lipoate-protein<br>conserved hypot | flagellar motor<br>insecticyanin B<br>insecticyanin A | flagellar motor sw<br>androgen-dependent<br>insecticyanin - to |                                    |
|                                  | Gaps  |                                      |  |                                    | 43718;  |   |  |  | for  | -1999   |  |            | phosphoes<br>cal prote<br>hypothet                             | biosynthes<br>protein li<br>d hypothet                 | ВВ  | motor sw<br>Rependent<br>Inin - to                             | and pepti<br>and pepti<br>motor sw |
|                                  | 0;  |                                      |  |                                    | PID:g132  |   |  |  | cell g   |   |  |            | ተወይጠ   | r + +· S   | ٤   | 0 ┌ ₹  | ₹ 1. 1.                            |
|                                  |   |                                      |  |                                    | 132   |   |  |  | grov   |   |  |            |  |  |   |  |                                    |

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A;Reference number: Z21751
A;Accession: T37881
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-144 <SKE>
A;Cross-reference
                                                                                        R;Ford, R.A.; Bhattacharjee, J.K.
Curr. Genet. 28, 131-137, 1995
A;Title: Molecular properties of the lys1(+) gene and the A;Reference number: S57264; MUID:96020159; PMID:8590464
A;Accession: S57264
                                                                                                                                                                                                                                                                                     RESULT 4
S57264
    A;Cross-references: EMBL:U15923 C;Keywords: oxidoreductase
                                                                                                                                                                                                                        L-aminoadipate-semialdehyde dehydrogenase (EC 1.2.1.31) - fission yeast (Schizosaccharom C;Species: Schizosaccharomyces pombe C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C. Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein At2g05260 [imported] - Arabidopsis thaliana (C;Species: Arabidopsis thaliana (mouse-ear coress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: E84466
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A; Introns: 131/3
C; Superfamily: mitochondr:
C; Keywords: mitochondrion
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A;Experimental source: strain
C;Genetics:
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C;Accession: T37881
R;Skelton, J; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V. submitted to the EMBL Data Library, August 1997
                                           A; Residues: 1-470 <FOR>
                                                             A; Molecule type: DNA
                                                                                A; Status: preliminary
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A; Residues: 1-358 <STO>
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position: 2
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41.7%;
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Library, August 1997
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1.1e+02;
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41;
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T01757
hypothetical protein A_IG002P16.20 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_
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A; Introns: 6/2;
A; Note: F8M12.9
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submitted to the Protein Sequence Database, A; Reference number: 215261
A; Accession: T04290
A; Molecule type: DNA
A; Residues: 1-665 <BEV
A; Cross-references: EMBL:AL049525
A; Experimental source: cultivar Columbia; BA
C:Genetics:
                                                                                                                                  A; Introns: 22/2; 2:
A; Note: F25I24.160
                                                                                                                                                                                                                                                                                                               R; Bevan, M.; Hilbert, H.; Braun, M.; Holzer,
                                                                                                                                                                                                                                                                                                                             hypothetical protein F25124.160 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Decies: Arabidopsis thaliana (mouse-ear cress) C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 30-Apr-1999 C;Accession: T04290
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A;Molecule type: DNA
A;Residues: 1-649 <MADD>
A;Cross-references: EMBL:AF080118; NID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F8M12.9 - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #C; Accession: T01882 R; Madsen, C.; Graves, T.; Cotton, M.; Modde, T. submitted to the EMBL Data Library, July 1998 A; Description: The sequence of A. thaliana F8M12.
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A;Experimental source: cultivar Columbia
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1.5e+02;
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March 1999
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#text\_change

22-Oct-1999

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conserved hypothetical protein [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 15-Jun-2001 C;Accession: A90413
R;She, O; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Reddarrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Postdues: 1-1174 <SCH>
A; Residues: 1-1174 <SCH>
A; Cross-references: EMBL:AL389890; GSPDB:GN00116; NCSP:B24P7.280
A:Pynorimental source: BAC clone B24P7; strain OR74A
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A, Description: The sequence of A. thaliana IG002P16.
A, Reference number: Z14421
A, Accession: T01757
A, Status: translated from GB/EMBL/DDBJ
A, Molecule type: DNA
A, Residues: 1-1133 <MIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: acetate-CoA ligase homology; acyl carrier protein homology C;Keywords: carrier protein F;71-610/Domain: acetate-CoA ligase homology <ACL> F;634-705/Domain: acyl carrier protein homology <ACP>
A; Reference number: A99139
A; Accession: A90413
A; Status: preliminary
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A; Map position: 6
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A; Accession: T50973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Schulte, U.; Aign, V.; submitted to the Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable alpha-aminoadipate reductase large subunit [imported] - Neurospora crassa N;Alternate names: protein B24P7.280
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A; Introns: 56/3; 92/3; 246/3; 288/3; 334/2; 532/1; 599/1; 641/1;
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R; Miller, N.; Beck,
                                                                      A; Description: Sulfolobus solfataricus complete genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Sequence Database,
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Pred. No.
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Pred. No. 3.8e+02;
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base, July 2000
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4e+02;
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R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrern as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junquelira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Lauchado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A.Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawal A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A., Saval A; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Aimeida, S.; Vettore, A.L., A;Reference number: A59328
                                                                                                                                                                                                                                   C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997
C;Accession: C69832
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R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below A;Accession: A82691
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A; Cross-references: GB:
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu,
                                                                                                             R;Kunst, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G; Azevedo, V.; Ber
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
                                                                                                                                                                                                                                                                                                                           methyl-accepting chemotaxis protein homolog yhfv -
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A; Residues: 1-257 <SIM>
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Best Local
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nes 5; Conservation
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nilarity 41.7%;
Conservative
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Pred. No. 1.2e+02;
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M.; Holsappel, S.; H
M.; Kurita, K.; I
Levine, A.; Liu,
                                                                                                                                                                                                                                                                 #text_change 20-Jun-2000
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Hosono, S.; H
Lapidus, A.;
L, H.; Masuda,
                                                                                    S.; Galizzi, A.; Gal
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y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; A; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A.;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A; Reference number: A69580; MUID:98044033; PMID:9384377
A; Accession: C69832
A; Status; preliminary; nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
A; Residues: 1-432 < KUN>
A; Molecule type: DNA
A; Residues: 1-529 <WIL>
A; Cross-references: EMBL: Z83107; PIDN: CAB05500.1; GSPDB: GN00019; CESP: F32A7.4
A; Experimental source: clone F32A7
C; Genetics:
                                                                                                                                                  submitted to the EMBL Data Library, November 1996 A; Reference number: Z19451 A; Accession: T21623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein PA5393 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: E82973
R;Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M. adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K. i, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                      hypothetical protein F32A7.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21623
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A;Experimental source: strain PAO1
C;Genetics:
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A; Residues: 1-450 <STO>
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Best Local Similarity
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A;Experimental source: strain 168
C;Genetics:
A;Gene: yhfy
C;Superfamily: Pyrococcus horikoshii probabl
                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                 R; Kershaw, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
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nes 5; Conserv
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41.7%;
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41.7%;
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Pred. No.
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Pred. No.
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2.1e+02;
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2.2e+02;
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K.; Lim,
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cytokinin oxidase 1
C;Species: Zea mays
C;Date: 12-Feb-1999
C;Accession: T01500
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A; Gene: ckx1
A; Introns: 20
                                                                                                                                                                                                                       R;Houba-Herin, N.; Pethe, C.; D'Alayer, J.; Laloue, M. Plant J. 17, 615-626, 1999
A;Title: Cytokinin oxidase from Zea mays: purification, A;Reference number: 25869
A;Accession: T51929
A;Status: preliminary; translated from GB/EMBL/DDBJ
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T51929
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                              δÃ
                                                                                                                                                                                                                                                                                                                          cytokinin oxidase [imported] - maize
c;Species: Zea mays (maize)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C;Accession: T51929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession. Accession. Accession of the EMBL Data Library, January 1998 submitted to the EMBL Data Library, January 1998 remainded cytokinin oxidase from maize.
                                                                                                                                A;Gene:
                                                                                                                                                           A; Experimental source: cultivar nobilis
                                                                                                                                                                             A; Residues: 1-534 <HOU>
A; Cross-references: EMBL:Y18377; PIDN:CAA77151.1
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A;Residues: 1-534 <MOR>
Ā;Cross-references: EMBL:AF044603; NID:g3341977;
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A; Map position: 1
A; Introns: 27/3; 60/2;
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5; Conserv
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                                                                 Conservative
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(maize)
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Pred. No.
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Pred. No. 2.7e+02
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Result
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GUN_CYFLMU
GUN_CYFLM
GUYA_CLOAB
MSII_AFATH
MSII_LYCES
ENO_ECOLI
ENO_SALTY
ENO_YERPE
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ENO_CHICK
ENO_HEICK
ENO_HEIC
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CARE MOUSE
CARE HUMAN
LYS2 CANAL
LYS2 SCHPO
HMAT BACSU
CKX1 MAIX
CKX1 ORYSA
CKX1 APLCA
ELHC APLCA
Y843 AQUAE
ELHA APLCA
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PIR; A36425; A36425.

SGD; S0003399; CLC1.

InterPro; IPR000996; Clathrin_lg_ch.

R Pfam; PF001086; Clathrin_lg_ch; 1.

DR PROSITE; PS00224; CLATHRIN_LIGHT_CHN_2; 1.

DR PROSITE; PS00581; CLATHRIN_LIGHT_CHN_2; 1.

Coated pits; Calcium-binding; Calmodulin-binding; Coiled coil.

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TRUCTURES.

TORAIN SPECIFIC INSERT IN LCA/LCB
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InterPro; IPR001767
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                            PROSITE; PS00657; FORK_HEAD_1; 1.
PROSITE; PS00658; FORK_HEAD_2; 1.
PROSITE; PS50039; FORK_HEAD_3; 1.
Hypothetical protein; Transcription regulation;
Nuclear protein.
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ProDom; PD000425; TF_Fork_head; 1.
SMART; SM00339; FH; 1.
                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kikuno R., Nagase T., Ishikawa K.-I., Hirosawa M., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; Tanaka A., Kotani H., Nomura N., Ohara O.; Prediction of the coding sequences of unidentified human genes. The complete sequences of 100 new cDNA clones from brain which co for large proteins in vitro."; DNA Res. 6:197-205(1999).

-I. SUBCELLULAR LOCATION: Nuclear (Potential).
-I. SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
                                                                                                                                                                                                                                                   InterPro; IPR001766; TF_Fork_head.
Pfam; PF00250; Fork_head; 1.
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Mammalia; Eutheria;
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Eukaryota; Metazoa; (
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Nunez G.;
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MEDLINE-21391892; PubMed-11387339;

MCAllister-Lucas L.M., Inohara N.,

Li Q., Chen S., Chen F.F., Yamaoka
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15-JUN-2002 (Rel. 41, Created)
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15-JUN-2002 (Rel. 41, Last annotation
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                                                                                                                               coil.
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                                                                                                                                              PS00856; GUANYLATE_KINASE_1; PS50052; GUANYLATE_KINASE_2; PS50106; PDZ; 1.
                                                                                                                                                                                                              PS50209; CARD; 1
                                                                                                                                                                                                                                                        IPR000619; Guanylate_kin.
IPR001478; PDZ.
                                       15
125
572
854
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                   107
411
655
986
743
    113496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to the EMBL/GenBank/DDBJ databases.
tes NF-kappaB via Bcll0 and IKK.
and Bcll0 bind to each other by CARD-CARD
  MW;
CARD.
COILED COIL (POTENTIAL).
PDZ.
GUANYLATE KINASE.
QAQQQLLA -> HLLEDHRS (IN R
QAQQQLLA -> HLLEDHRS (TR R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                       FALSE_NEG.
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                                                                                                                                                                                                                                                                                                                                                                                 noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein kinase C activation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
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erma I.M., Mak T.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
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                        REF.
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                        2).
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Query Match

Score

36;

DВ

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CARE_HUMAN
ID CARE_H
AC Q9BXL6
AC CELARD14
AC Q9BXL6
AC ACRD14
AC CARD14
AC ACRD14
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                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restructed by non-profit institutions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE-21255663; PubMed-11356195;
Gaide O., Martinon F., Micheau O.,

"Carmal, a CARD-containing binding
phosphorylation and NF-kappaB activ
FEBS Lett. 496:121-127(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21192234; PubMed=11278692;
Bertin J., Wang L., Guo Y., Jacobson M.D., Poyet J.-L.,
Srinivasula S.M., Merriam S., DiStefano P.S., Alnemri E.S.;
"CARD11 and CARD14 are novel caspase recruitment domain
(CARD)/membrane-associated guanylate kinase (MAGUK) family members
that interact with Bc110 and activate NF-kappaB.";
J. Biol. Chem. 276:11877-11882(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R. Submitted (DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O9BXIG; Q9BVB5;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                   use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2) (Carma 2).
CARD14 OR CARMA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Cervix,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-740 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERRATUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caspase recruitment domain protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEBS Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109
                                                                                                                                                                                                                                                                                                                                                                                                                      Interaction.

SUBCELLULAR LOCATION: Cytoplasmic.

SUBCELLULAR LOCATION: Expressed in placenta. Also determined the subcept of the placenta. Also determined the subcept of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
FUNCTION: Activates NF-kappaB via Bcll0 and IKK. Stimulates phosphorylation of Bcll0.
SUBUNIT: CARD14 and Ballo Expenses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIDESTESGLME 120
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                                      AY032927;
BC018142;
BC001326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                AF322642;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Martinon F., Micheau 505:198-198(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
; AAG53403.1; -.
; AAK6453.1; -.
; AAH18142.1; -.
; AAH181326.1; ALT_INIT.
; AGH01326.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12
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Primates;
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nding partner of
activation.";
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Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.
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14 (CARD-containing
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                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                   There are no rest
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i; Hominidae;
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Bcll0,
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induces Bcll0
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYS2_CANAL Q12572;
                                      This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and modified and this statement is not removed.
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DOMAIN
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SMART; SM00228; PD2; 1.

PROSITE; PS00209; CARD; 1.

PROSITE; PS00856; GUANYLATE_KINASE_1;

PROSITE; PS50052; GUANYLATE_KINASE_2;

PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                               Suvarna K., Seah L., Bhattacherjee V., Bhattacharjee J.K.; "Molecular analysis of the LYS2 gene of Candida albicans: homology to
                                                                                                                                                                                                                                                                                                           STRAIN-ATCC 11651 / B792;
                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota;
Saccharomycetales; mitosporic
                                                                                                                                                                                                                                                                                                                                                                              Candida albicans (Yeast).
                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Aminoadipate-semialdehyde dehydrogenase large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                 -!- COFACTOR: CONTAINS 1
                                                                                                                                                                                                                                                                                                      MEDLINE=98228267; PubMed=9560434;
                                                                                                                                                                                                                                                                                                                                                                                                     (Alpha-aminoadipate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coiled
                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=5476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001478; PDZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 DXDXSXFXGXXQ
                                                                                                        SIMILARITY: CONTAINS 1 ACYL CARRIER DOMAIN.
                                                                                                                             SIMILARITY).
SIMILARITY:
                                                                                                                                                   SUBUNIT: HETERODIMER
                                                                                                                                                             PATHWAY:
                                                                                                                                                                        (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DVDFSNFSGLME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1004
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128
568
858
619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                Lysine biosynthesis;
HETERODIMER OF AN ALI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                              BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
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409
658
990
                                                                                                                                                                                                                                                                                                                                                                                                   reductase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.3%;
41.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113299
                                                                                                                             TO
                                                                                                                                                                                  COVALENTLY BOUND PHOSPHOPANTETHEINE
                                                                                                                             THE ATP-DEPENDENT AMP-BINDING ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GUANYLATE KINASE.
DYEASEPLFKAYLEDTTLEEAVGLLRRVDGFCCLSVKVNTD
DYEASEPLFKAYLEDTTLEEAVGLLRRVDGFCCLSVKVNTD
GYKRLLQDLEAK -> SRARPLLSPGLLMGTVAAGGVTQAD
GYKRLLQDLEAK -> SRARPLLSPGLLMGTVAAGGVTQAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARD.
COILED
PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FTSPRRCRSTLGWASALSWADVKRSAHL (IN
                                                                                                                                                                                                                                                                                                                                                        Saccharomycotina; :
Saccharomycetales;
                                                                                                                                                   ALPHA AND
                                                                                                                                                                                                                                                                                                                                                                                                  (Alpha-AR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7469B8B56BE06073 CRC64;
                                                                                                                                                              sixth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1391
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                                                                                                                                                step.
D A BETA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΑĀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                               subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1004;
                                                                                                                                                                                                                                                                                                                                                          Saccharomycetes;
; Candida.
                                                                                                                                                   SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                               (EC
                                                                                                                                                                                                                                                                                                                                                                                                               1.2.1.31)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                          collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).

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           RA Wood V. Gwilliam R. Majandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brown D., Brown S., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., McLean J.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., McLean J.,
RA Holroyd S., Hornsby T., Jones M., Leather S., McDean J.,
RA Holroyd S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Galbart R., Cullins S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Woodward J., Vonstreels E., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vonstreels E., Rieger M., Scheefer M., Mueller-Auer S.,
RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Cerrutti L., Lowe T., McComble W.R., Paulsen I., Potashkin J.,
RA Shakwyski G. V. Urser P., Resper D., Harrell B., Benito J.,
RA Schaffer R., Radalland R., Radalsen I., Potashkin J.,
RA Schaffer R., Radalsen I., Potashkin J.,
RA Schaffer V., McComble W.R., Paulsen I., Potashkin J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYS2_SCHPO STANDARD; PRT; 1419 A P40976; Q9P770; 01-FEB-1995 (Rel. 31, Created) 16-OCT-2001 (Rel. 40, Last sequence update 15-JUN-2002 (Rel. 41, Last annotation upda Aminoadipate-semialdehyde dehydrogenase (E aminoadipate reductase) (Alpha-AR).

LYS1 OR SPAP7G5.04C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; P1408/; LAND.
InterPro; IPR000873; AMP-bind.
InterPro; IPR003880; Ppantine_attach.
Pfam; PF00501; AMP-binding; 1.
Pfam; PF00550; pp-binding; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; FALSE_NEG.
PROSITE; PS00015; AMP_BINDING; 1.
PROSITE; PS000455; AMP_BINDING; 1.
PROSITE; PS50075; ACP_DOMAIN; 1.
Lysine biosynthesis; Oxidoreductase; NADP; Phosphopantetheine.
Lysine biosynthesis; Oxidoreductase; NADP; Phosphopantetheine.
DOMAIN 852 902 PHOSPHOPANTETHEINE (POTENTIAL).
PROSITE: PS000184 884 884 PHOSPHOPANTETHEINE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ford R.A., Bhattacharjee J.K.; "Molecular properties of the lys1+ gene and the regulation aminoadipate reductase in Schizosaccharomyces pombe."; Curr. Genet. 28:131-137(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-21848401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Curr. Genet. 28:13
[2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96020159; PubMed=8590464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DXDXSXFXGXXQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DLDWSGYRGAIQ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
    Ussery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=11859360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                      Thode G.,
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Best Local S
Matches 5
                                                                                  15-JUN-2002 (Rel. 15-JUN-2002 (Rel. 15-JUN-2002 (Rel. 15-JUN-2002 (Rel. Heme-based aerotac
                                                                                                                                                                                                                                                                                 CONFLICT
CONFLICT
CONFLICT
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CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                         Lysine biosynthesis; Oxidoreductary DOMAIN

RRS
                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
PROSITE;
                                       Bacillus subtilis.
Bacteria; Firmicutes;
NCBI_TaxID=1423;
                                                                                                                                                 BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature
  STRAIN=168;
Noback M.A.
                     SEQUENCE FROM
                                                                                                                           007621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000873; AMP-bind.
InterPro; IPR003880; Ppantne_at
Pfam; PF00501; AMP-binding; 1.
Pfam; PF00550; pp-binding; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U15923; AAC15909.1;
EMBL; AL353014; CAB88271.
HSSP; P14687; IAMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a or send an email to
                                                                         HEMAT
                                                                                                                                     HMAT_BACSU
                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                    BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: CONTAINS 1 ACYL CARRIER DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- PATHWAY: Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- COFACTOR: CONTAINS 1 COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- CATALYTIC ACTIVITY: L-2-aminoadipate 6-semialdehyde + NADP(+) H(2)O = L-2-aminoadipate + NADPH.
                                                                                                                                                                                                             1 DXDXSXFXGXXQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: CATALYZES THE ACTIVATION ATP-DEPENDENT ADENYLATION AND THE F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALPHA-AMINOADIPATE BY NADPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genome sequence of Schizosaccharomyces re 415:871-880(2002).
                                                                                                                                                                                        DLDWSGYRGAIQ
                                                                                                                                                                                                                                  Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
                                                                                   aerotactic
                                                                                                                                                                                                                                                                                                                            916
916
196
187
500
600
620
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lysine biosynthesis; IY: BELONGS TO THE AT
 Terpstra
                      N.A.
                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CAB88271.1;
                                                                                            41,
                                                                                                                                                                                                                                                                                    953
916
91
196
487
500
602
621
712
928
1205
                                                                                                                                                                                                                                                                                                                                                                                                                                          AMP_BINDING; 1. ACP_DOMAIN; 1.
                                                                                                                                                                                                                                          92.3%;
41.7%;
                                                                                                                                                                                                                                                                                                                                                                                                            Oxidoreductase; NADP; Phosphopantetheine 53 ACYL CARRIER (ACP).
                                                                                                                                                                                                                                                                           156893
                                                                                                                  Created)
 P.,
                                                                                   transducer
                                                                                           Last sequence up
Holsappel
                                                                                                                                                                                                                                                                    MW;
                                                                                                                                                                                                                                                                                                     PHOSPHOPANTETHEINÉ (POTE MT -> IA (IN REF. 1).
MISSING (IN REF. 1).
D -> DG (IN REF. 1).
R -> G (IN REF. 1).
MISSING (IN REF. 1).
MISSING (IN REF. 1).
AR -> GP (IN REF. 1).
Y -> SG (IN REF. 1).
VVV -> AAA (IN REF. 1).
VVV -> AAA (IN REF. 1).
                                                                                                                                                                                                                                          Score 36; I
Pred. No. 1
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                                                                                                                                                                                                                                                                                              LVRM -> WSK
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; 09AFBEFE09F21A0C CRC64;
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ATP-DEPENDENT
                                                                                                                                                                                                                                  Mismatches
                                                    Bacillaceae;
  s:
'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BOUND PHOSPHOPANTETHEINE
                                                                                                                                      432
                                                                                            update)
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  Venema
                                                                                                                                                                                                                             JB 1,
1.6e+02;
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             as its content
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  o.
ز
                                                                                                                                                                                                                                                    Length 1419;
                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
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                                                                                                                                                                                                                                 Gaps
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the EMBL/GenBank/DDBJ databases

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RA Azevedo V. Bertero M.G. Bessieres P. Bolotin A. Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borrist S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Crarai E., Foulger D.,
RA Choi S.K., Codani J.J., Connerton I.F., Crarai E., Foulger D.,
RA Choi S.K., Codani J., Rosinet C., Ferrari E., Foulger D.,
RA Choi S.K., Caller P., Goffeau A., Golightly E.J., Grandi G.,
RA Gliseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Gliseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kurita K., Lapidus A., Lardinois S., Hullo M.F., Itaya M., Jones L.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sekiguchi J., Seanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sato T., Takashashi H., Takemaru K.,
RA Yoshida K., Yahamoto H., Yahane K., Yasumoto K., Yata K.,
RA Yoshida K., Yahamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yatashachot H., Yamane K., Yasumoto K., Yata K.,
Rh Yoshida K., Yatashachot H., Yamane K., Yasumoto K., Yata K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Resonance Raman and ligand binding studies of the oxygen-sensi signal transducer protein HemAT from Bacillus subtilis.";
J. Biol. Chem. 277:13528-13538(2002).
-i' FUNCTION: Heme-containing signal transducer responsible for aerotaxis, the migratory response toward or away from oxyge-i- SUBUNIT: Homotetramer (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hou S., Larsen R.W., Boudko D., Riley C.W ordal G.W., Alam M.;
"Myoglobin-like aerotaxis transducers in Nature 403:540-544(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                             SubtiList; BG13066; hemAT.
InterPro; IPR004089; Chmtaxis_transd
                                                                                             SMART; SM00283; MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aono S., Kato T., Matsuki M., Nakajima H., Ohta T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESONANCE RAMAN SPECTROSCOPY, AND SUBUNIT MEDLINE=21950695; PubMed=11821422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20140131; PubMed=10676961;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS
                                                                                                                                   PF00015; MCPsignal;
                                                                                                                                                                                                                                                                       Y14084; CAA74545.1; -. Z99109; CAB12878.1; -.
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87D0655974070B64 CRC64;
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RESULT 8
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1. FUNCTION: Catalyzes the oxidation of cytokinins, a family of N(6)-substituted adenine derivatives that are plant hormones, where the substituent is an isopentenyl group.

1. CATALYTIC ACTIVITY: N6-(3-methylbut-2-enyl)adenine + H(2)O + adenine + 3-methylbut-2-enpl + H(2)O(2).

1. COFACTOR: FAD (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jusaki T., Matsumoto T., Submitted (JUL-2000)
                                                                                                                                                                                                                                Pfam; PF01565; FAD_binding_4; 1.
PROSITE; PS00862; OX2_COVAL_FAD; 1.
                                                                                                                                                                                                                                                                     EMBL; AP002836; BAB07927.1; EMBL; AP002816; BAB03420.1;
                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=cv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CKX1_ORYSA
                                                                                                                                                                             BINDING
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                                                                                                                                                                                                                       Oxidoreductase;
                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probable cytokinin oxidase precursor (EC 1.4.3.18) (CKO). P0512G09.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
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                                                                                                                                                                                                                                                                                                                                                            European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Extracellular (By similarity). SIMILARITY: Belongs to the oxygen-dependent FAD-linked
                                                                                                                                                                                                                                                                                                                                                                                                                 oxidoreductase family.
                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
DFDRGVFKGILQ
                                                 Similarity 5; Conser
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                                                             Score 35;
Pred. No.
                                                                                                                                                                               PROBABLE CYTOKININ OXIDASE. FAD (COVALENT) (BY SIMILARITY).
                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                    FAD; Signal; Glycoprotein
                                                                                                    B849D646E3BB4A7E CRC64;
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                                                            . 83;
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                                                                                               Oxidoreductase;
                                                                                                                                                                                                                              EMBL; Y18377;
EMBL; AF04460;
                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sibor send an email to license@isb-sib.ch).
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AND MASS SPECTROMETRY.
MEDLINE=99160863; PubMed=10049708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Houba-Herin N., Pethe C., D'Alayer J., Laloue M "Cytokinin oxidase from Zea mays: purification, expression in moss protoplasts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SEQUENCE O STRAIN=cv. Nobilis; TISSUE-Kernel; MEDLINE=99246676; PubMed=10230061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; El
Spermatophyta; Magnoliophyta; Liliopsida;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                      MaizeDB; 194080;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION, AND TISSUE SPECIFICITY MEDLINE=21068113; PubMed=11154345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plant Physiol. 125:378-386(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 255:328-333(1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays (Maize).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: Catalyzes the oxidation of cytokinins, a family of N(6)-substitutted adenine derivatives that are plant hormones, where the substituent is an isopentenyl group. Cleaves zeatin, isopentenyladenine, isopentenyladenosine, zeatin riboside and ciszeatin, but not dihydrozeatin, kinetin and benzylaminopurine. CATALYTIC ACTIVITY: N6 (3:methybut-2-enyl)adenine + H(2)0 + O(2) adenine + 3-methylbut-2-enal + H(2)0(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: Glycosylated, with SIMILARITY: Belongs to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: Monomer (By similarity).
SUBCELLULAR LOCATION: Extracellular.
TISSUE SPECIFICITY: Expressed in imm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oxidoreductase family.
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E; PS00862; OX2______,

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                                                                              Pro; 1970007, IPRO01575; Oxid_FAD_bind.
PF01565; FAD_binding_4; 1.
TE; PS00862; OX2_COVAL_FAD; 1.
reductase; Flavoprotein; FAD; Signal; Glycoprotein.
                                                                                                                                                                                                                              AF044603;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and biochemical characterization of a cytokinin
                                                                                                                                                                                                                                                          CAA77151.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            approximately 10 hexose residues per
the oxygen-dependent FAD-linked
                     CYTOKININ OXIDASE POLY-ALA.
                                                                         POTENTIAL
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a; Poales; Poaceae; PACC clade;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369-377;
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                                                                                                                                                                                        Pfam; PF02156; Glyco_hydro_26; PRINTS; PR00739; GLHYDRLASE26.
                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Politz O., Krah M., Borriess R.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-beta-D-mannosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=ATCC 43812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhodothermus marinus (Rhodothermus Bacteria; Bacteroidetes; Sphingobac Crenotrichaceae; Rhodothermus.
                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                  EMBL; X90947; CAA62442.1;
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                                                                                                                                                                                                                            InterPro; IPR000805;
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16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                            linkages in mannans, galactomannans, glucomannans, and galactoglucomannans.
SIMILARITY: BELONGS TO FAMILY 26 OF GLYCOSYL HYDROLASES.
EADRSVFRGLAQ
                                                                                                                                                                         lase;
                                                                                             Similarity
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1021 AA; 11
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                                                                                               89.7%;
41.7%;
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Pred. No.
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N-LINKED (GLCN
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-> F (IN REF. 2).
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                                                                            Mismatches
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83;
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ELHB\_APLCA ID ELHB\_A AC P11924

ELHB\_APLCA P11924;

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                                                                                                                                                                01-OCT-1989
01-OCT-1989
15-JUN-2002
                                                                                                                                                                                                                            _APLCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nagle G.T., Painter S.D., Blankenship J.E., Dixon J.D., Kurosky A.;
"Evidence for the expression of three genes encoding homologous
atrial gland peptides that cause egg laying in Aplysia.";
J. Biol. Cohem. 261:7853-7859(1986)
-i- FUNCTION: INJECTED IN SEXUALLY MATURE ANNIMALS CALIFIN B EXCITES
LB AND LC CELLS OF THE ARDOMINAL GANGLION AND CAUSE EGG-LAYING.
-i- SUBUNIT: THIS PROTEIN CONSISTS OF A LARGE 36-RESIDUE SUBUNIT,
BOUND BY A SINGLE DISCUFTIDE-BOND TO A SMALL 18-RESIDUE SUBUNIT.
-i- MISCELLANEOUS: CALIFIN B PROBABLY DERIVES FROM POLYPROTEIN B,
WHICH IS ALSO THE PRECURSOR FOR PEPTIDE B.
-i- SIMILARITY: TO ELH/ACIDIC PEPTIDE.
PIR; B26295; B26295.
PIR; D26306.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rothman B.S., Hawke D.H., Brown R.O., Lee T.D., Dehghan Shively J.E., Mayer1 E., "Isolation and primary structure of the califins, three active egg-laying hormone-like peptides from the atrial aplysia californica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1989
01-OCT-1989
15-JUN-2002
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Eukaryota; Metazoa; Mollusca;
Aplysiidae; Aplysia.
NCBI_TaxID=6500;
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MEDLINE=86224083; Pu
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MEDLINE=86111826; pubMed=3753705;
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          "Isolation and primary structure of the califins, three biologically active egg-laying hormone-like peptides from the atrial gland of
                                   TISSUE-Atrial gland;
MEDLINE-86111826; PubMed=3753705;
Rothnan B.S., Hawke D.H., Brown R.O., Lee
Shively J.E., Mayeri E.;
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                                                                                                                                                                                                                                                                                              1 DXDXSXFXGXX
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41,
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                                                                                                                             (California sea hare).
Mollusca; Gastropoda;
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36 LARGE SUBUNIT
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Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
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45.5%;
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annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                     SMALL SUBUNIT
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                                                                                                                               Opisthobranchia; Anaspidea;
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SEQUENCE
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"Byddence for the expression of three genes encoding homologous
atrial gland peptides that cause genes encoding in Aplysia.";
J. Biol. Chem. 261:7853-7859(1986).
-i- FUNCTION: INJECTED IN SEXUALLY MATURE ANIMALS CALIFIN C EXCITES
LB AND LC CELLS OF THE ABDOMINAL GANGLION AND CAUSE EGG-LAYING.
-i- SUBUNIT: THIS PROFEIN CONSISTS OF A LARGE 36-RESIDUE SUBUNIT.
-I- SUBUNIT: TO ELH/ACIDIC PEPTIDE.
InterPro; IPR003442; UPF0079.

Pfam; PF02367; UPF0079; 1.

TIGRFAMS; TIGR00150; UPF0079; 1.

Hypothetical protein; ATP-binding; Complete proteome.

NP_BIND
36
43
ATP (POTENTIAL).

SEQUENCE 133 AA; 15246 MW; 45C990DED12C4138 CRC64;
                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQUAE
                                                                                                                                                                                                                                                                          MEDLINE=98196666; PubMed=9537320;
Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y843_AQUAE
067011;
                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bacteria; Aquificae;
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PIR; C26306; C26306.
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                                                                                   EMBL; AE000710; AAC06981.1;
                                                                                                                                                                                                                        Nature 392:353-358(1998).
-!- SIMILARITY: BELONGS TO THE UPF0079 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000
16-OCT-2001
                                                                                                                                                                                                                                                                "The complete genome of the hyperthermophilic
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hormone; Neuropeptide;
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RESULT 14

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P01360; p11923;
21-JUL-1986 (Rel. 01, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-AUG-1990 (Rel. 15, Last annotation update)
Atrial gland peptide A precursor (ELH-18) [Contains: Califin A].
Aplysia californica (California sea hare).
Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Isolation and primary structure of the active egg-laying hormone-like peptides Aplysia californica.";
J. Biol. Chem. 261:1616-1623(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mayeri E., Axel R.; "A single gene encodes multiple neuropeptides mediating a stereotyped hahavior.":
                                                                                                                                                                                                                                                                                                    "Proteolytic processing of 
Aplysia. Identification of
                                                                                                                                                                                                                                                                                                                          Nagle G.T., Painter S.D., Blankenship J.E., Kurosky A., "Proteolytic processing of egg-laying hormone-related p
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 22-34; 131-152 AND 156-173. MEDLINE-88243802; PubMed-3379066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rothman B.S., Hawke D.H., Brown R.O., Lee T.D., Dehghan A.A., Shively J.E., Mayeri E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Atrial gland;
MEDLINE=86111826; PubMed=3753705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Purification and primary structure of two neuroactive processes and call afterdischarge and egg-laying in Aplysia. Proc. Natl. Acad. Sci. U.S.A. 77:2328-2332(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 36-69 (PEPTIDE A). MEDLINE-80190239; PubMed-6929554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Structure and expression of the egg-laying hormone gene family in Aplysia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aplysiidae; Aplysia.
NCBI_TaxID=6500;
                                                                                                                                                                                                                                               J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 117-173 (CALIFIN A).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cell 32:7-22(1983)
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                      BIOL. Chem. 263:9223-9237(1988).

FUNCTION: THE ATRIAL GLAND PEPTIDE A & PEPTIDE B PRECURSORS ARE TURE SOURCE OF THE 2 PEPTIDES THAT, UPON RELEASE FROM THIS REPRODUCTIVE SYSTEM GLAND, INITIATE THE EGG-LAYING PROCESS BY EXCITING THE BAG CELL NEURONS. THESE NEURONS, CLUSTERED IN NEURAL CONNECTIVES NEAR THE ABDOMINAL HEADLION, IN TURN RELEASE OTHER PEPTIDES THAT ACT DIRECTLY ON THE GANGLION & ALSO, VIA THE CIRCULATING HEMOLYMPH, ON MANY OTHER ORGANS TO CONTROL THE PHYSIOLOGICAL PROCESSES OF EGG-LAYING. ONE OF THESE OTHER PEPTIDES
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THE EGG-LAYING
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Pred. No.
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DE Flagel
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OC Bacter
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RA Gene 1
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Q57259;
15-DEC-1998 (
15-DEC-1998 (
15-JUN-2002 (
Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Wood Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordo Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W.
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PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae; Rhizobium.
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15-DEC-1998 (Rel. 37, Last sequence up
15-DUN-2002 (Rel. 41, Last annotation
Flagellar motor switch protein flin.
FLIN OR FILN OR ATT0562 OR AGR_C_988.
                                                                                                                                                                                                                                                                          MEDLINE-97305159; PubMed-9161425;
Deakin W.J., Parker V.E., Loake G.J., Shaw C.H.;
"The Agrobacterium tumefaciens motor gene, mota, cluster with the flagellar switch protein genes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                             MEDLINE=21608550; PubMed=11743193; Wood D.W., Setubal J.C., Kaul R., Monks D.E.,
                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        Gene 189:139-141(1997).
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$L; J01017; AAA27742.1;

$L; A01630; GOGAAA.

$L; A26295; A26295;

$L; B28108; B28108.
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45.5%;
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CS -> PQLK
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Pred. No.
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ATRIAL GLAND PEPTIDE A.
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MIDATION (G-153 PROVIDE AMIDE GROUP
S -> POLKTENILD (IN REF. 2).
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RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Flanagan C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.,
RA Gielo C., Slater S.,
Ra Grenome sequence of the plant pathogen and biotechnology agent
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58.";
RScience 294:2323-2328(2001).
R. Science 294:2323-238(2001).
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Best Local S
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EMBL; U63390; AAC45323.1; -.
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EMBL; AE009025; AAL41579.1; -.
EMBL; AE007990; AAK86374.1; ALT_INIT.
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PRINTS; PR00956; FLGMOTORFLIN.
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                                                                                                                                                                                                                                                                                                                                     Complete proteome. SEQUENCE 179 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=21608551; PubMed=11743194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The genome C58.";
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45.5%;
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## SUMMARIES

| 16     | 15                 | 14                | 13                 | 12                | 11                | 10                 | . 9    | œ                  | 7                 | 100                | U                  | 4                  | . ω                | N                  | , 11               | Result<br>No.    |
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| Q8RX19 | Q9SJ35             | 8 A L A 6 0       | Q8SUF6             | Q95RB4            | Q8T8Q9            | 013813             | Q94KI4 | Q94KI5             | Q95P90            | Q92JT3             | Q9N076             | Q9GM13             | Q9NQ76             | Q95KG5             | Q99QK6             | ID               |
|        | Q9sj35 arabidopsis | Q9vjy8 drosophila | Q8suf6 encephalito | Q95rb4 drosophila | Q8t8q9 drosophila | Ol3813 schizosacch |        | Q94ki5 triticum ae | Q95p90 mesobuthus | Q92jt3 rhizobium m | Q9n076 macaca fasc | Q9gm13 macaca fasc | Q9nq76 homo sapien | Q95kg5 macaca fasc | Q99qk6 streptomyce | Description      |

| 44<br>45                                 | 43     | 42     | 41                 | 40                | 39                 | 38     | 37      | 36     | ა<br>5  | 34                 | 33     | 32                 | 31      | 30     | 29     | 28                 | 27                 | 26     | 25                | 24                | 23     | 22     | 21     | 20     | 19     | 18                 | 17                 |
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| Q90w20 hippoglossu<br>O33220 mycobacteri |        |        | Q8rph9 desulfitoba | Q9hei9 neurospora | Q91xw2 mus musculu |        | $\circ$ |        |         | Q42526 arabidopsis |        | Q90646 gallus gall |         | a      |        | Q9pdk6 xylella fas | Q981z3 rhizobium l |        | Q97w30 sulfolobus | Q9p3q7 neurospora | $\sim$ |        |        |        |        | 081620 arabidopsis | Q8rjp2 erwinia chr |

## ALIGNMENTS

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Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q99QK6 PRELIMINARY; PRT; 272 AA.
Q99QK6;
Q09QK6;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein SCP1.337c.
SCP1.337C AND SCP1.17.
                                                                                               "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL590464; CAC35862.1; -.
EMBL; AL590463; CAC35539.1; -.
Hypothetical protein; Plasmid.
SEQUENCE 272 AA; 29985 MW; 2D7D6D25B936E9E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces coelicolor. Plasmid SCP1.
                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. NCBI_TaxID=1902;
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1 DXDXSXFXGXXQ 12
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ EMBL; AB060891; BAB46894.1; -.
Hypothetical protein.
Hypothetical protein.
SEQUENCE 500 AA; 55577 MW; 918D265AD8EDC71
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Q95KG5;
Q1-DEC-2001 (TremBlrel. 19, Created)
Q1-DEC-2001 (TremBlrel. 19, Last sequence update)
Q1-DEC-2001 (TremBlrel. 19, Last annotation update)
Q1-DEC-2001 (TremBlrel. 19, Last annotation update)
Hypothetical 55.6 kDa protein.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                    EMBL;
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01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                             hypophosphatemic osteomalacia, is expressed Genomics 74:342-351(2001).
EMBL; AJ276396; CAB97250.1; -.
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Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=21309068; PubMed=11414762;
Argiro L., Desbarats M., Glorieux F.H.,
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TISSUE-TEMPORAL LOBE RIGHT;
                                                     CHAIN
                                                                                                                                                                                                                                                                                    Argiro L., Desbarats M., Glorieux F.H., Ec "Mepe, the gene encoding a tumor-secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20399567; PubMed=10945470; Rowe P.S.N., De Zoysa P.A., Dong R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEPE
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Primates;
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              MATRIX EXTRACELLULAR PHOSPHOGLYCOPROTEIN. 0977CA6E871CA9E5 CRC64;
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                                                                                 POTENTIAL
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01-MAR-2001
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                                                                                                                                               libraries.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ
EMBL; AB046056; BAB01638.1;
                                                                                                                                                                                                           SEQUENCE FROM N.A.
OSADA N., Hida M., Kusuda J., Tanuma R.,
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones fro
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Macaca fascicularis (Crab eathing macacue) (Cynomolgus monkey).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostc

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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01-OCT 2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          libraries.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ Submitted (OCT-2000) to the EMBL/GenBank/DDBJ FMBL; AB050259; BAB17010.1; - RD4D47E88038A9
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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Osada N., Hida M., Kusuda J., Tanuma F
Suzuki Y., Sugano S., Hashimoto K.;
Tisolation of full-length cDNA clones
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Q95990 ID P9599 AC Q959 AC Q959 DT 01-D DT 01-D DT 01-D DT 01-D DE Puta OS Mesc CO Buth OX NCBI RN CI I RN CI I SQ S Du SEQU SQ SEQU SQ SEQU
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Q1-DEC-2001 (TrEMBLrel. 19, C:
Q1-DEC-2001 (TrEMBLrel. 20, L:
Q1-MAR-2002 (TrEMBLrel. 20, L:
Hypothetical protein R03146.
R03146 OR SMC03761.
                                                                                                                                                                                                 035p90;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
putative toxin-11ke peptide KTXLP2.
Mesobuthus martensii (Manchurian scorpion) (Buthus r
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachn
Buthoidea; Buthidae; Buthus.
                                                                          Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Bolstard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Godrie T., Coffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F., "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium mellioti strain 1021.", Sinorhizobium mellioti strain 1021.", Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
EMBL; AL591793; CAC47725.1; InterPro; IPR001410; DEAD. InterPro; IPR001401; DEAD. InterPro; IPR001650; Helicase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00270; DEAD; 1.
Pfam; PF00271; helicase_C; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 1832 AA; 202209 MW; 23053AE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                      Q95P90
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                                                  Local Similarity
nes 5; Conserv
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                       1 DXDXSXFXGXXQ 12
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Pred. No. 3.2e+02;
6; Mismatches 0;
                                                                 Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                    PRT;
                                                    Mismatches
                                                                                                                                                                                                                                                scorpion) (Buthus martensii).
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01-JUN-2002
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Q94KI4;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Cytokinin dehydrogenase (Fragment).
Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooldear
Triticeae; Hordeum.
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SEQUENCE FROM N.A.
Galuszka P., Frebort I., Sebela M., Yamada M., Pec P.,
Galuszka P., Frebort I., Sebela M., Yamada M., Pec P.,
"Cloning of the genes encoding cytokinin dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF362472; AAK51495.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Galuszka P., Frebort I., Sebela M., Yamada M., Pec P.; "Cloning of the genes encoding cytokinin dehydrogenase in barley.";
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
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Galuszka P., Frebort I., Sebela M., Yamada M.,
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16 DEDRAVERGILQ 27
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137
137 AA;
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137 AA;
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Pred. No.
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Pred. No. 54;
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                             Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases EMBL; AY075572; AAL68378.1; -. SEQUENCE 251 AA; 27011 MW; FA95DB8BD5146935 CRC64;
                                                                                                                                                                  Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: CENTRAL COMPONENT OF THE RECEPTOR COMPLEX RESPONSIBLE
FOR THE RECOGNITION AND TRANSLOCATION OF CYTOSOLICALLY SYNTHESIZED
MITOCHONDRIAL PREPROTEINS (BY SIMILARITY).
-I- SUBUNIT: FORMS PART OF THE RECEPTOR COMPLEX THAT CONSISTS OF AT
LEAST 8 DIFFERENT PROTEINS (BY SIMILARITY).
-I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MITOCHONDRIAL
OUTER MEMBRANE (BY SIMILARITY).
-I- SIMILARITY: TO YEAST TOM22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative mitochondrial import receptor subunit (Mitochondrial 22 kDa outer membrane protein) (Translocase of outer membrane 22 kDa subunit) (MASI7 protein) (Mitochondrial 17 kDa assembly protein).
                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                       Patel S., Ph
Celniker S.;
                                                                                                                                                                                                                                                                                                                            Drosophila
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  194
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37 DSDESDFEGLEE
DGDGAQFYGQQQ 205
                             DXDXSXFXGXXQ 12
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5; Conserv
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                                                         Conservative
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n; Transmembrane.
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                                                                      92.3%;
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41.7%;
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                                                                    Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8AA1823E28C6989E CRC64;
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                                                         Mismatches
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57;
                                                                    1.1e+02;
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01-DEC-2001
01-DEC-2001
01-MAR-2002
LD46333p.
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01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Chawez C., Dorsett V., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                     Hypothetical protein SEQUENCE 308 AA;
                                                                                                                                "Genome sequence and gene compaction Encephalitozoon cuniculi."; Nature 414:450-453(2001).
EMBL; AL590449; CAD25784.1; -.
                                                                                                                                                                                                                                                                   Delbac F., El Alaoui H., Peyr
Weissenbach J., Vivares C.P.;
                                                                                                                                                                                                                                                                                                  MEDLINE-21576510; PubMed-11719806; Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F., Prensier G., Barbe V., Peyretaillade E., Brottier P., Wincker P., Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Microsporidia; NCBI_TaxID=6035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical
ECU10_0650.
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InterPro; IPR001965; Znf_PHD.
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NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q95RB4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genoscope
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                                                                     F09148E030A0EEC2 CRC64;
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Length 308;
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RESULT
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RA Addams M.D., Celniker S.E., Holt R.A., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Haril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Marvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Mattei B., McIntosh T.C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Merkulov G., Wilshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Renington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Abnert K., Renington K.A., Stapleton M., Skupski M.P., Shih H.T.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Shih H.T.,
RA Sher E., Spradling A.C., Stapleton M., Skupski M.P., Shih H.T.,
RA Kaliliams S.M., Woodage T., Worler S., Wang S., Yao Q.A.,
RA Kaliliams S.M., Woodage T., Worley K.C., Wu S., Zhu X., Smith H.O.,
RA Shen S. S., Saveri J. Shong W., Zhou X., Shith H.O.,
RA Shen S. S., Saveri J., Zhong W., Zhou X., Shith H.O.,
RA Shen S. S., Saveri S., Shong G., Zhou X., Smith H.O.,
RA Shen S. Saveri S., Shong
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Q9VJY8;
Q1-MAY-2000
Q1-MAY-2000
Q1-MAR-2002
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CG9293.
                                                                                                                                                                                                                                             "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
EMBL; AE003640; AAF53297.1; -.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                              Pfam; PF00628; PHD; 1
                                                                                                                                                                                     InterPro; IPR001965; Znf_PHD
                                                                                                                                                                                                                      FlyBase; FBgn0032516; CG9293.
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                                                                                                                          SM00249;
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                                                                                         ; 1.
37051 MW; OB6BC8F0684891B7 CRC64;
92.3%;
41.7%;
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7; Mismatches 0;
Score 36; DB 5;
Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S., Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter J.C.; "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                        Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AC007018; AAD29063.1; .
InterPro; IPR002921; Lipase_3.
InterPro; IPR002052; NG_Mtase.
Pfam; PF01764; Lipase_3; 1.
PROSITE; PS00092; NG_MTASE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  At2g05260 protein AT2G05260.
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                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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STRAIN=CV. COLUMBIA;
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                                                                                                                                                                                                                                    Conservative
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41.7%;
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                                                                                                                                                                                                                                                            Score 36;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                   694F8F5E5B9A6116 CRC64;
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                                                                                                                                                                                                                                                            DB 10;
1.8e+02;
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edons; core eudicots; Rosidae;
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                                                                                                                                                                                                                                                                                       Length 358;
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Gill J.E.,
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